Lithocholic bile acid, an aging-delaying natural compound, alters the pattern of protein phosphorylation in quiescent and non-quiescent cells of *Saccharomyces cerevisiae*

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ABSTRACT

Lithocholic bile acid, an aging-delaying natural compound, alters the pattern of protein phosphorylation in quiescent and non-quiescent cells of Saccharomyces cerevisiae

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Our laboratory has previously used a high-throughput screening of commercial compound libraries to discover several natural chemicals that delay chronological aging of the baker's yeast *Saccharomyces cerevisiae*. One of these chemicals is a lithocholic bile acid. We have previously shown that lithocholic acid delays yeast chronological aging by crossing the plasma membrane, accumulating in both mitochondrial membranes and remodeling lipid metabolism in mitochondria. The resulting changes in the mitochondrial membrane lipidome alter mitochondrial functionality and convert mitochondria into a signaling compartment. This signaling compartment modulates a distinct set of transcriptional factors that respond by eliciting specific changes in the transcription of many nuclear genes. The resulting changes in the cellular proteome create an aging-delaying cellular pattern because they affect many cellular processes, including an age-related death of quiescent and non-quiescent cell populations. All these aging-delaying changes that take place in yeast exposed to lithocholic acid suggest that this bile acid promotes a complex cascade of events affecting many other cellular processes. Regulated changes in reversible protein phosphorylation have been implicated in the control of many cellular processes. I sought to make a first step towards understanding how the regulated protein phosphorylation may delay yeast chronological aging in response to lithocholic acid treatment. To attain this objective, in studies described here, I used mass spectrometry-assisted proteomics to investigate possible changes in protein phosphorylation patterns within purified populations of quiescent and non-quiescent yeast cells treated with

lithocholic acid. My findings indicate that lithocholic acid elicits specific changes in the protein phosphorylation pattern of quiescent and non-quiescent yeast cells.

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Introduction

1.1. Baker's yeast is a valuable model organism to study mechanisms of cellular aging

The budding yeast *S. cerevisiae* is a eukaryotic, unicellular organism that has a short chronological lifespan and a well-defined life cycle (Longo et al. 2012; Arlia-Ciommo et al. 2014). It has been used as a model organism in various aging studies which have revealed the underlying biological components and mechanisms implicated in the delay of cellular aging and extending longevity (Longo et al. 2012; Arlia-Ciommo et al. 2014). Specifically, this yeast has been key in the discovery of the following: 1) decreased activation of certain signaling pathways such as TOR/Sch9 pathway and Ras/cAMP/PKA pathway which both regulate yeast metabolism by responding to changes in nutrient availability can extend chronological lifespan in yeast, 2) dietary interventions such as calorie restriction, done by reducing the percentage of glucose in the growth medium, is a chronological life extending property in yeast and 3) several chemical compounds such as lithocholic acid, which is thought to act independently of the TOR and cAMP/PKA pathways, that are able to extend yeast chronological lifespan when coupled with caloric restriction (Arlia-Ciommo et al. 2014). It has also led to the developing concept that chronological aging progresses through various checkpoints in a stepwise fashion, involving several metabolites and signaling protein complexes (Arlia-Ciommo et al. 2014). It is evident that the knowledge on cellular mechanisms gained from the study of *S. cerevisiae* proves it to be a valuable model organism. The discovery of these genes, signaling networks, dietary interventions and chemical compounds in *S. cerevisiae* has also created a foundation for the study of the intricacy of cellular aging in multicellular eukaryotes such as nematodes, fruit flies, mice and primates (Fontana et al. 2010).

Indeed, aging studies involving more complex eukaryotes have revealed that reduced activity of the nutrient-sensing pathway TOR/S6K (S6K being the equivalent of Sch9 in other eukaryotes), is involved in extending chronological lifespan in worms, and flies, additionally the reduced activity of the Ras/cAMP/PKA signaling pathway has similar effects on monkeys (Fontana et al. 2010). Specifically, the reduction of TOR and S6K kinases activity increases lifespan of worms, flies and mice (Fontana et al. 2010). Secondly, calorie restriction, the reduction of food intake without malnutrition, has lifespan extending properties in rodents and primates (Fontana et al. 2010). From this, it can be shown that the mechanisms of biological aging and its delay have been evolutionarily conserved across species.

1.2. Lithocholic acid (LCA) delays aging of baker's yeast and selectively kills cultured human cancer cells

Through a high-throughput screen of 24 geroprotective small molecules, the Titorenko lab has recently discovered that lithocholic acid (LCA) delays chronological aging in yeast under caloric restriction when added exogenously (Medkour et al. 2017). LCA is a mammalian bile acid which is produced by microflora within the gastrointestinal tract (Gafar et al. 2016). Like other bile acids, this secondary compound has been reported to have anti-neoplastic and anti-carcinogenic properties, showing toxicity to human cancer cells without affecting normal cells at low concentrations and the ability to trigger apoptotic pathways (Gafar et al. 2016). LCA has also been shown to have the highest delaying effects on chronological aging under caloric restriction via a mechanism that is not dependent on nutrient availability but rather targets lipid metabolism and transport within the cell (Arlia-Ciommo et al. 2018). To note, other plant and microbial

geroprotectors such as caffeine, resveratrol and rapamycin also have age delaying effects on chronological lifespan, however they modulate signaling pathways that are controlled by nutrient availability and therefore only show these effects under non-caloric restricted conditions (Medkour et al. 2017).

In the last few years, the Titorenko lab has provided evidence that LCA effects aging through the following mitochondrial properties: 1) LCA is able to cross the cell wall and plasma membrane and is stored within the mitochondria, 2) LCA increases the size of mitochondria and decreases the total number of mitochondria found within the yeast cell, 3) LCA decreases the relative concentrations of non-bilayer forming classes of phospholipids, 4) LCA alters concentrations of mitochondria proteins which are essential for certain mitochondrial functions 5) LCA modifies mitochondrial respiration, the maintenance of membrane potential, preservation of ROS homeostasis and ATP synthesis, 6) LCA increases the phospholipid to phosphoprotein ratio in mitochondrial membranes, 7) LCA increases the concentration of PA which stimulates mitochondria fusion, 8) LCA causes changes in phospholipid classes which increases mitochondrial cristae that connect in the mitochondria matrix as flat bilayers, disconnecting from IMM (Arlia-Ciommo et al. 2018). Furthermore, through a hypothetical model, the Titorenko lab has proposed that LCA also effects chronological aging by altering the concentrations of the proteins outside of the mitochondria (Arlia-Ciommo et al. 2018).

The proposed model by the Titorenko lab outlines the possible mechanism by which LCA delays chronological aging in yeast cells with the following key points: 1) by altering the communication between certain lipid and carbohydrate metabolism intermediates, LCA causes the development and maintenance of the an age delaying cellular pattern, 2) LCA causes a shift towards mitochondria fusion, instead of fission, 3) the development and maintenance of an age

delaying cellular pattern and shifting towards mitochondria fusion decreases cells committing to death via liponecrotic and apoptotic RCD modes in the post-diauxic and stationary phases, which increases the chances of cell survival, 4) Since LCA decreases the risk of age-related death, it prolongs longevity in chronological aging yeast, 5) LCA decreases the cellular concentration of FFA in chronological lifespan by accelerating TAG synthesis from FFA in the ER, ensuring the deposit of TAG within lipid droplets and by decelerating TAG lipolysis into FFA, 6) LCA stimulates the transport of acetyl-CoA from peroxisomal to mitochondria via carnitine shuttle, 7) in a similar way, LCA stimulates the transport of pyruvate from cytosol to mitochondria, 8) the transport of acetyl-CoA and pyruvate to the mitochondria may be involved in the remodeling of mitochondrial lipidome and changes in overall mitochondrial function (Mitrofanova et al. 2018; Arlia-Ciommo et al. 2018).

Notably, the mechanism through which LCA cytotoxicity works on human cancer cells have shown that LCA selectively kills cultured human neuroblastoma, prostate and breast cancer cells by first triggering an ER stress response and an autophagic response (Gafar et al. 2016). The activation in such pathways then induces ROS and mitochondrial dysfunction (Gafar et al. 2016). Since the activation of stress responses via the ER, mitochondria and autophagy are heavily involved in the anti-neoplastic and anti-carcinogenic properties of LCA, the study of LCA can be of interest in the field of anti-aging and cancer therapy. Specifically, the structure of bile acids, such as LCA, can from the basis for the development for selective drugs treatments.

1.3. Purification, properties and aging of quiescent and non-quiescent populations of *S. cerevisiae* cells

After glucose exhaustion, a yeast culture has the ability to differentiate into two cell populations; one existing in the state of quiescence and the other having a state of non-quiescence (Leonov et al. 2017). Quiescence is the temporary state of non-proliferation. Research has shown that in the state of quiescence, cells are able to suppress cell division without affecting the ability to re-enter the cell cycle (Mohammad et al. 2019). This prevents the cell from becoming senescent or from entering a state of terminal differentiation (Mohammad et al. 2019). Quiescent cells are able to re-enter the cell cycle and proliferate in response to external signals and regulatory mechanisms (Mohammad et al. 2019). Cells in this population are mainly daughter cells that are uniform in size, are resistant to long-term oxidative and thermal stress and have a delayed onset of programmed cell death (Leonov et al. 2017). To note, quiescence is also a property of stem cells amongst multicellular organisms (Mohammad et al. 2019). Particularly, mammalian quiescent cells are able to support resistance to different stressors and toxicities and self-renew through infrequent and asymmetrical division into a daughter progenitor (Mohammad et al. 2019). Non-quiescence is a terminal state in which cells are mitotically active (Leonov et al. 2017). This population of cells are primarily mother cells that are highly reproductive and are committed to becoming apoptotic, necrotic or senescent (Leonov et al. 2017). The purification of quiescent and non-quiescent cell populations is achieved by separating these cells by their density. Quiescent cells are high in density, whereas non-quiescent cells are low in density (Leonov et al. 2017).

Entry to the quiescent state is known to be controlled by the regulation of the cell cycle as well as the metabolic status of the cell at the different phases of the cell cycle (Mohammad et al. 2019). Furthermore, the regulation of the differentiation of quiescent and non-quiescent cells has been thought to be involved in extending lifespan under caloric restriction through a mechanism

that links this process to cellular aging and cell regulation (Mohammad and Titorenko 2018). Recently, the Titorenko lab has shown that under caloric restriction quiescent and non-quiescent cell populations are both composed of stem cell niches which play a role in this mechanism (Mohammad and Titorenko 2018). The cells found in these subpopulations are non-differentiated, viable, unbudded and arrested in G0, a specialized non-proliferative of the G1 phase in the cell cycle (Mohammad and Titorenko 2018). It is thought that the mechanism by which caloric restriction can delay chronological aging is composed of four distinct processes which modulates the differentiation of quiescent and non-quiescent cells (Mohammad and Titorenko 2018). First, under caloric restriction the formation of the stem cell subpopulation occurs in early G1, as opposed to later in G1 when under non-caloric restrictions (Mohammad and Titorenko 2018). Second, quiescent cells of high density commit to differentiate into quiescent cells of low density in the logarithmic phase under caloric restriction, instead of in the stationary phase if under non-caloric restrictions (Mohammad and Titorenko 2018). Finally, the differentiation of cells is shifted towards quiescent cells as opposed to non-quiescent cells (Mohammad and Titorenko 2018). This is achieved in two ways. Under caloric restriction, the differentiation of quiescent low density cells forms non-quiescent low density cells and the advancement of quiescent cells through a maintenance program also forms non-quiescent cells (Mohammad and Titorenko 2018). To increase the abundance of quiescent cells both progression through the differentiation program and the advancement in the maintenance program are decreased (Mohammad and Titorenko 2018). From this it can be understood that the mechanism in which caloric restriction extends yeast chronological lifespan is done by regulating and maintaining the abundance of cells in the non-proliferative, quiescent state. It should be noted the number and functionality efficiency of quiescent cells declines with age and changes associated to aging in stem cell niches are an

essential contribution in the age-related decline in the ability of stem cells to retain their properties though molecular signaling (Mohammad et al. 2019). Since the efficiency of stem cell niches to produce molecular signals are enhanced or weakened with age, the mechanisms controlled by these niches contribute to age related decrease in stem cell functionality (Mohammad et al. 2019).

1.4. Reversible protein phosphorylation controls many cellular processes

The ability of complex life to survive and thrive relies heavily on its ability to process and respond to constantly changing internal and external cues/environment (Humphrey et al. 2015). To account for this, cellular processes are tightly controlled by the phosphorylation of cellular proteins (Humphrey et al. 2015; Ardito et al. 2017; Arlia-ciommo and Arlia-ciommo 2018). Phosphorylation is a reversible post-translational modification which acts as a backbone for almost every cellular processes, hence the involvement of phosphorylation in the regulation of metabolism, cell division, cell growth, cell development and overall cellular aging (Ardito et al. 2017). More specifically, the role of phosphorylation within a cell is tied to its ability to function as a molecular switch, a modulator of temporary protein-protein interaction and to trigger changes in protein conformation and subcellular localization of its substrates (Humphrey et al. 2015; Ardito et al. 2017). All of these functions compose the intricate and specific relationship between phosphorylation and intra and extracellular communication/signal transduction (Humphrey et al. 2015; Ardito et al. 2017).

The ways in which phosphorylation drives cellular communication is based on the direct and indirect activation and deactivation of integral proteins to signaling networks by protein kinases and phosphatases (Humphrey et al. 2015; Ardito et al. 2017). An example of a signaling pathway that is heavily reliant on phosphorylation is the PI3k/Akt/mTOR signaling pathway

(Humphrey et al. 2015; Xu et al. 2020). The first phosphorylation event occurs after an extracellular growth factor binds to a receptor tyrosine kinase causing this kinase to autophosphorylate and through a cascade of phosphorylation events activates PI3k, which in the same manner activates Akt (Xu et al. 2020). Akt promotes cell proliferation and inhibits apoptosis (Xu et al. 2020). Downstream of Akt is mTOR, which aids in protein synthesis, cell cycle progression and decreases the occurrence of apoptosis as well (Xu et al. 2020). Akt activates mTORC1 through the inactivation of mTORC1 inhibitors through their phosphorylation (Humphrey et al. 2015). Like many cellular pathways, the relationship between Akt and mTOR is not unidirectional. Instead, once mTORC1 is active it starts a series of phosphorylation events that leads to the feedback inhibition of Akt (Humphrey et al. 2015). Though the regulation of metabolism by cellular signaling revolves around this switch-like mechanism, it has been revealed that signaling can also regulate metabolism in the same manner (Humphrey et al. 2015). Akt goes through an ATP-dependent allosteric change in conformation which regulates access to inhibitory phosphatases, and therefore kinase activity is a function of cellular ATP levels (Humphrey et al. 2015).

Another example of a kinase cascade that is dependent on phosphorylation is the MAPK pathway. Similar to the Akt/mTOR pathway, MAPK is activated by a series of phosphorylation events that are initiated by the binding of an external growth factor to a membrane protein, which in turn causes a downstream activation of kinases (Wei and Liu 2002; Ardito et al. 2017). Ultimately, this leads to the regulation of gene expression (Wei and Liu 2002; Ardito et al. 2017).

The study of protein phosphorylation (phosphoproteomics) is a valuable tool in understanding cellular mechanisms and the regulatory functions of their kinases. This is especially helpful in the study of the mechanisms involved in tumor formation. Since phosphorylation is one

of the most common PTMs involved in the regulation of many biological processes and overexpression of kinases, phosphorylation is heavily involved in the onset and development of oncogenesis (Ardito et al. 2017). Ras and mTOR are both proteins which are characterized by phosphorylation events and their activation is common in mammalian cancers (Ardito et al. 2017). For this reason, phosphoproteomics plays an important role in tumor biology and cancer therapies. Specifically, inhibitors of pathway kinases are looked to as drug treatments (Ardito et al. 2017).

1.5. Mass spectrometry-based phosphoproteomics is used to investigate mechanisms through which reversible protein phosphorylation controls many cellular processes

A proteome is defined as the collection of all the proteins under particular conditions (Choudhary and Mann 2010). A phosphoproteome, then, can be defined as all the proteins that have undergone the post-translational modification of phosphorylation at a given state. In 2016, it was estimated that approximately one to two-thirds of an organism's proteome is regulated by phosphorylation (Vlastaridis et al. 2017). Data reported on the saccharomyces genome database estimates that in yeast this amounts to about 2500 phosphoproteins and PhosphoGrid2 estimates that within the yeast proteome there is anywhere between 15 000 and 21 000 phosphorylation sites (Vlastaridis et al. 2017). Compared to the human proteome which is estimated to contain about 3500 phosphoproteins and about 86 000 phosphorylation sites (Vlastaridis et al. 2017). These estimations only provide a general idea of the vastness that still needs to be discovered and can provide ideas for new approaches that need to be developed to complete a proteome (Vlastaridis et al. 2017). The paradox within this field lies in the fact that a complete phosphoproteome, let alone a proteome can only be formed once all proteins have been identified and there are no longer any novel sites discovered.

Mass spectrometry has become an innovative tool in discovering phosphoproteins, as well as the cellular processes they regulate. A prime example is the MAPK signaling pathway, which Lopez et al. describe as a dynamic system that can be better understood through MS-based phosphoproteomic tools (López et al. 2012). As previously mentioned, the MAPK signalling pathway is heavily regulated by a cascade of phosphorylated kinases, however the authors specifically mention that the interaction with small G-protein coupled receptors connects the MAPK modules to external stimulus via cell surface receptors (López et al. 2012). Since phosphoproteomic studies are able to identify proteins that are phosphorylated at specific times and spaces, the finer details of this pathway could potentially be characterized (López et al. 2012).

The method for mass spectrometry lies in this universal workflow: extracting the proteome, enriching for specific proteins of post-translational modifications, separating the proteins into peptides, ionizing the peptides, obtaining the mass spectra and fragments of the peptides and finally analyzing the acquired data from this multi-step process (Choudhary and Mann 2010). A simple way of extracting and separating proteins from yeast cells is to subject the proteome to polyacrylamide gel electrophoresis (Choudhary and Mann 2010). Proteins within the gel can then be subject to digestion with proteases such as trypsin (Choudhary and Mann 2010). To obtain the phosphoproteome, phosphoproteins within a proteome can be enriched by metal oxide affinity chromatography (MOAC) using porous TiO_2 beads (Aryal and Ross 2010; Eyrich et al. 2011). The interaction between the beads and phosphoprotein occurs from the affinity of the oxygen in the phosphate group for the TiO2 metal atoms (Aryal and Ross 2010). Although there are alternatives to MOAC and TiO2, such as immobilized metal-ion affinity chromatography (IMAC) this method is less selective and common, yielding low recoveries for phosphorylated proteins (Aryal and Ross 2010; Eyrich et al. 2011). All the purified peptides are then separated on a reverse phase

chromatography column, and the eluted peptides are ionized by electrospray (Choudhary and Mann 2010). A spectrum of all these peptides is acquired to obtain their mass and intensity, which is referred to as the mass spectrum (MS) mode (Choudhary and Mann 2010). Each eluted peptide is then isolated and fragmented a second time by a force of energy strong enough to break chemical bonds (Choudhary and Mann 2010). This is referred to as the MS/MS spectrum (Choudhary and Mann 2010). A compiled list of the mass and fragment masses for each peptide is scanned against a protein sequencing database which then gives a list of peptides and proteins (Choudhary and Mann 2010). The inference of proteins detected from peptides can be drawn from a peptide spectrum match (PSM) (Frank 2009). A PSM refers to the pairing of an identified mass spectrum to a peptide fragment (Frank 2009). The number of peptide spectrum matches refers to the total number of peptide and mass spectrum pairs recorded by the mass spectrometer. This number is larger than that of the number of phosphorylated proteins since several peptide fragments may be identified multiple times (Frank 2009). The resulting protein list can then form the basis for biological discovery by mass-spectrometry (Choudhary and Mann 2010).

1.6. The objective of studies described in this thesis

The objective of studies described in this thesis was to make a first step towards understanding how regulated protein phosphorylation may delay yeast chronological aging in response to lithocholic acid treatment. To attain this objective, in studies described here, I used mass spectrometry-assisted proteomics to investigate possible changes in protein phosphorylation patterns within purified populations of quiescent and non-quiescent yeast cells treated with lithocholic acid.

Materials and Methods

2.1 Yeast strain, media and growth conditions

Wild-type (WT) strain *Saccharomyces cerevisiae* BT4742 (MATα his3-Δ1 leu2-Δ0 lys2-Δ0 ura3-Δ0) from Thermo Fisher Scientific was grown in YP medium (1% yeast extract, 2% peptone) initially containing 0.2% (w/v) glucose with 50μM LCA or without it. Cells were cultured at 30°C with rotational shaking at 200rmp in Erlenmeyer flasks with a "flask volume/medium volume" ratio of 5:1.

2.2. Separation of quiescent and non-quiescent cell populations by Percoll density gradient centrifugation

2 ml of 1.5 NaCl and 16ml of Percoll solution was placed into a 50ml conical polypropylene centrifuge tube and mixed by pipetting. 4ml of the NaCl/Percoll mixture was put into four polyallomer tubes for an MLS-50 rotor for an Optima MAX ultracentrifuge to form four Percoll density gradients. The tubes were centrifuged at 25 000 x g for 15 min at 4°C at an Optima MAX ultracentrifuge. A sample of yeast cells, untreated and treated with LCA, were collected on days 0, 1, 2, 5, and 7 of culturing. A fraction of the sample was diluted in order to determine the total number of cells per milliliter of culture using a hemocytometer. For each Percoll density gradient, ~ 1 x 10^9 yeast cells were placed into 15ml conical polypropylene centrifuge tube and pelleted by centrifugation at 5000 rpm for 7 minutes at room temperature. Pelleted cells were resuspended in 500μl of 50 mM Tris/HCl buffer (pH 7.5) and overlaid onto the Percoll gradient. With the overlay, the Percoll gradients were centrifuged at 2,300 x g for 30 minutes at 25°C in an Optima MAX ultracentrifuge to obtain upper and lower fractions. These fractions were collected

into separate tubes with a pipette and Percoll was removed by washing the cells with 50 mM Tris/HCl buffer (pH 7.5) two times. The cells were resuspended in 50 mM Tris/HCl buffer (pH 7.5) for further analysis and stored in -80°C.

2.3. Protein preparation for digestion

2.3.1. Glass bead lysate

For cell lysis, untreated and treated cell fractions were centrifuged at 3,000 rpm for 60 seconds at room temperature and 50 mM Tris/HCL buffer (pH 7.5) was removed. The pellet was gently resuspended in 2% CHAPS lysis buffer (2% CHAPS in 25 mM Tris/HCl pH 8.5) twice and then subjected to vigorous shaking with glass beads for 10 minutes at 4°C. Lysates were pelleted by centrifugation for 5 min at 16 000 x g at 4°C and supernatant was collected in a pre-chilled Eppendorf tube.

2.3.2. Bradford protein assay

Bradford protein assay was used to estimate the amount of protein within each lysate. A bovine serum albumin (BSA) standard curve was prepared on the BioMate160 spectrophotometer by Thermo Scientific. Samples were added to 1ml of 1X Bradford Reagent, mixed by vortexing in an Eppendorf tube and incubated for 10 minutes at room temperature. The absorbance of each sample was read and recorded at 595 nm. Appropriate volumes were taken for each sample based off of the absorbance reading.

2.3.3. Protein precipitation

For phosphoproteomic mass spectrometry studies 200µg of proteins was taken from each sample. The extracted proteins were precipitated with 10% TCA and incubated on ice for 30

minutes. Each sample was centrifuged at 16,000 x g for 10 minutes at 4°C. The pellet was retrieved and washed with 80% acetone, dried and resuspended in the sample buffer for SDS-PAGE.

2.3.4. SDS-PAGE

To prepare the protein samples for digestion, each sample was resuspended in SDS-PAGE sample buffer (2% SDS, 10% Glycerol, 5 % β-mercaptoethanol, 0.005% bromophenol blue in 62.5 mM Tris/HCl (pH 6.8)) to obtain a final protein concentration of 1µg/µl and incubated at room temperature overnight. Samples were loaded to an SDS-polyacrylamide gel at 200V until a band was formed in the running gel. After staining the running gel with QC Colloidal Coomassie Blue and de-staining, protein bands were cut out from the SDS-PAGE gel with a razor blade.

2.3.5. Protein digestion and peptide extraction

Protein digestion and peptide extraction is optimized from the protocols provided by Concordia University's Centre for Biological Applications of Mass Spectrometry (CBAMS). For the first extraction, the gel pieces were placed in individual 1ml Eppendorf tubes and incubated in 10 mM dithiothreitol (DDT) for 30 mins at room temperature. DDT was discarded and the gel pieces were incubated in 50 mM iodoacetamide (IAA) for 30 min at room temperature in the dark. IAA was removed and the gel pieces were incubated in 50 mM ammonium bicarbonate (ABC) at room temperature for 15 minutes. The ABC was removed and the gel pieces were incubated in a mixture of 25 mM ABC with 5% acetonitrile (ACN) for 15 min at room temperature. The mixture was removed and the gel pieces were incubated with a mixture of 25 mM ABC and 50% ACN for 15 minutes at room temperature. The mixture was removed and the gel pieces were incubated under the same conditions. The mixture was removed and the gel pieces were incubated for 10 minutes with 100% ACN. Gel pieces were dried at 37°C and rehydrated with 0.01 µg/µl trypsin in 25 mM ABC solution and incubated overnight at 30°C. For the second extraction, the gel pieces

were incubated in 60% ACN and 0.5% formic acid for 15 minutes. The supernatant was collected and the previous step was repeated twice. The gel pieces were no longer used and discarded. The supernatant was dried, and the formed pellet was frozen at -20°C until preparation for Mass Spectrometry (MS) Analysis.

2.4. Phosphopeptide enrichment by TiO_2

Phosphopeptide enrichment protocol is provided by GE Healthcare Life Sciences. Peptides were re-dissolved in a binding buffer of 1M glycolic acid in 80% acetonitrile with 5% trifluoroacetic acid (TFA). Titanium dioxide (TiO_2) beads were equilibrated with binding buffer and the sample was added. Sample was then incubated for 30 minutes under 360° rotation, washed once with binding buffer, then again with 80% ACN and 1% TFA. The bound peptides were eluted twice from the beads using 5% ammonium hydroxide, pH 12. The phosphopeptide containing eluate was collected and dried.

2.5. Mass spectrometry

For phosphoproteomic analysis, peptides were re-dissolved in 15 µl of 2% acetonitrile and 1% formic acid before mass spectrometry analysis. The peptide mass and fragmentation were identified using label-free reverse-phase high performance liquid chromatography, coupled to tandem mass spectrometry using EASY-nLC™ II coupled to LTQ Orbitrap Velos. Each sample was subject to a total run time of 92 minutes, where each peptide was separated in an ACN gradient and with a constant sample elution of 400 nL per minute from a 100-µM capillary column packed with C18 mobile phase.

2.6. Software

Thermo Proteome Discoverer 2.4 and SEQUEST were used to search Saccharomyces cerevisiae databases, using custom workflows by CBAMS. Reported peptides and proteins have a set false discovery rate < 1%. Proteome Discoverer 2.4 (PD2.4) was also used to generate figures, such as principal component analysis (PCA) plot. The principal component analysis plot depicts the relationship of different samples to one another. Samples that lie physically near each other are the most similar. The component is chosen by PD2.4 software and cannot be changed. Microsoft Office was used to process the data exported PD2.4 for data analysis and presentation purposes.

Results and Discussion

3.1 Number of peptide spectrum matches and phosphorylated proteins

Mass spectrometry-based phosphoproteomics revealed the recovery of 300-700 phosphorylated proteins on different days of culturing (Fig 1). The number peptide spectrum matches (PSMs) obtained was 59 000-74 000. A larger number of PSMs than the number of proteins recovered may be an indication that the same peptide fragment was identified repeatedly. Based on phosphoproteome size, phosphoproteomes grouped by day vary by 200 phosphoproteins.

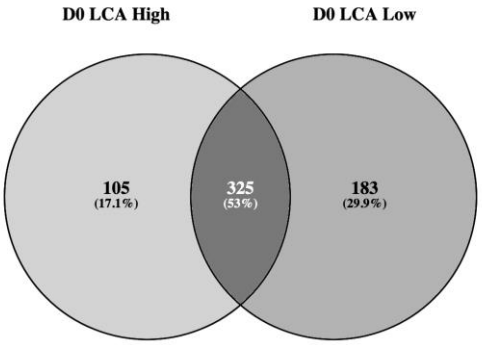
Timepoint	Treatment	Cell Population (Density)	Number of PSMs	Number of Phosphorylated Proteins
D0	Untreated	High	68 037	613
		Low	69 165	716
	LCA	High	63 638	430
		Low	66 518	508
D1	Untreated	High	72 029	657
		Low	64 533	480
	LCA	High	67 398	611
		Low	73 504	767
D2	Untreated	High	69 628	611
		Low	71 816	732
	LCA	High	70 287	683
		Low	70 605	691
D5	Untreated	High	67 150	504
		Low	65 986	439
	LCA	High	68 862	580
		Low	66 833	511
D7	Untreated	High	59 489	313
		Low	70 893	695
	LCA	High	74 120	799
		Low	71 147	650

Table 1. Table of the numbers of peptide spectrum matches (PSMs) and phosphorylated proteins found in Q and NQ yeast cells treated with LCA or remained untreated and taken on different days of culturing.

Phosphoproteins that are unique to a sample can provide insightful information to the pathways, organelles and cellular mechanisms that are being phosphorylated under certain conditions. Table 2 and Figures 2.1-2.5 outline the number of proteins that are unique to high density (quiescent) and low density (non-quiescent) yeast cells treated with LCA on different days of cultures. During day 0 and day 1, both days of the logarithmic phase, the number of unique proteins of low density untreated cells is larger than those of high density. During day 2, the number of unique proteins in both cell populations are similar. During day 5, a time point reflecting the post-diauxic phase, the phosphoproteome of high density cells contains double the number of unique proteins than that of the low density and day 7, a timepoint at which most cells are in stationary phase, the phosphoproteome of high density cells is four times larger than those of low density cells.

Timepoint	Cell Population (Density)	Total Number of Unique Proteins	Total Number of Proteins in Sample
D0	High	105	430
	Low	183	508
D1	High	80	611
	Low	236	767
D2	High	257	683
	Low	265	691
D5	High	141	580
	Low	72	511
D7	High	210	799
	Low	61	650

Table 2.1 Table of the number of phosphoproteins unique to high density and low density yeast cells treated with LCA and taken on different days of culturing.



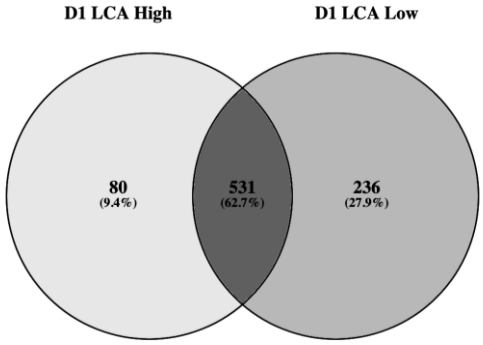
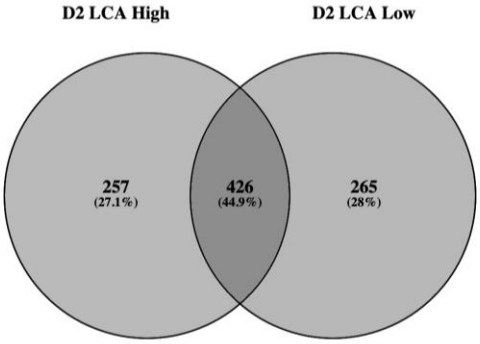


Figure 2.1 and Figure 2.2. Venn Diagram of the number
of phosphoproteins common and unique to high density and low density yeast cells treated with LCA and taken on day 0 and day 1.



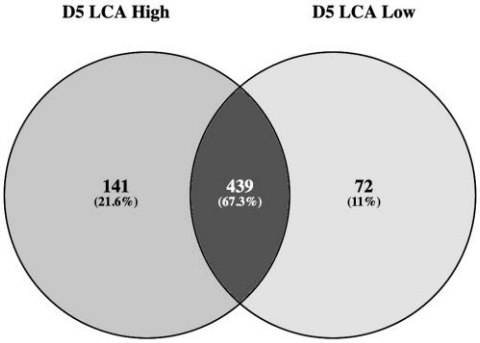


Figure 2.3 and Figure 2.4. Venn Diagram of the number of phosphoproteins common and unique to high density and low density yeast cells treated with LCA and taken on day 2 and day 5.

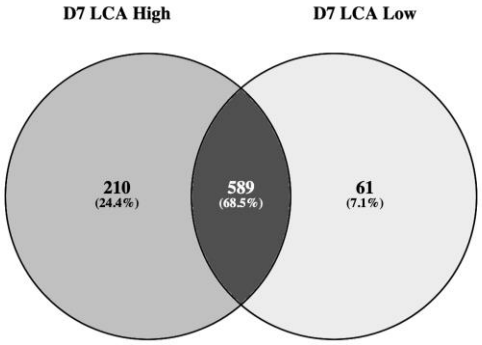
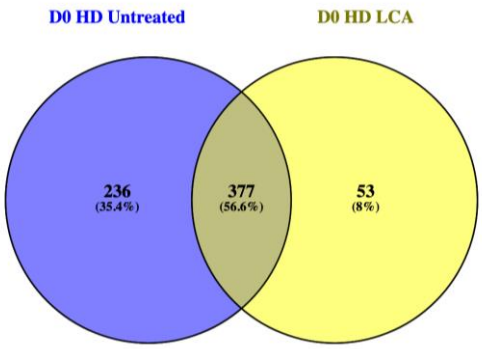


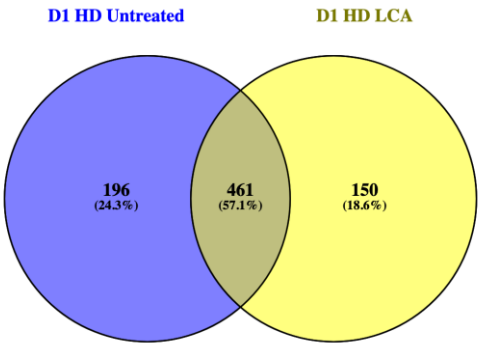
Figure 2.5 Venn Diagram of the number of phosphoproteins common and unique to high density and low density yeast cells treated with LCA and taken on day 7.

Table 2.2 and Figures 2.6-2.10 outline the number of proteins that are unique to high density (quiescent) yeast cells treated with or without LCA on different days of cultures. During day 0 and 1 the number of unique proteins of untreated high density cells is larger than those of cells treated with LCA. During day 2, the number of unique proteins in both cell populations are similar. During day 5, the phosphoproteome of high density cells treated with LCA contains double the number of unique proteins than that of the untreated cells and day 7 the phosphoproteome of high density cells is thirty times larger than those of low density cells.

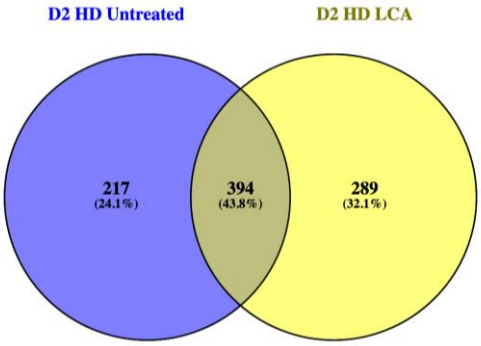
Timepoint	Color	Treatment	Total Number of Unique Proteins	Total Number of Proteins in Sample
D0		Untreated	236	613
		LCA	53	430
D1		Untreated	196	657
		LCA	150	611
D2		Untreated	217	611
		LCA	289	683
D5		Untreated	84	504
		LCA	160	580
D7		Untreated	17	313
		LCA	503	799

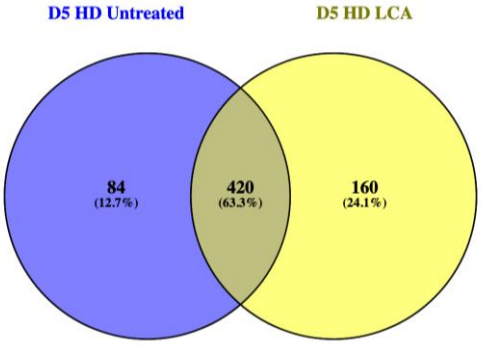
Table 2.2 Table of the number of phosphoproteins common and unique to high density yeast cells treated with LCA or remained untreated and taken on different days of culturing.



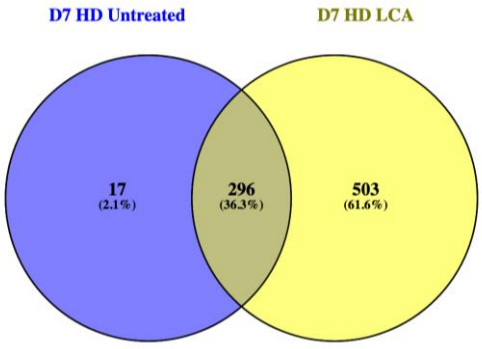


Figures 2.6 and 2.7. Venn Diagram of the number of phosphoproteins common and unique to high density yeast cells treated with LCA or remained untreated and taken on day 0 and day 1.





Figures 2.8 and 2.9. Venn Diagram of the number of phosphoproteins common and unique to high density yeast cells treated with LCA or remained untreated and taken on day 2 and day 5.



Figures 2.10. Venn Diagram of the number of phosphoproteins common and unique to high density yeast cells treated with LCA or remained untreated and taken on day 7.

3.2 Principal component analysis plot phosphorylated proteins

Phosphoproteome size shows the total number of proteins within a phosphoproteome. However, size is not the only way to compare phosphoproteomes. The data in the principal component analysis plot shows that samples that lie physically near each other on the plot are most similar. Each sample is identified on Figure 5 by day, density and treatment. To further characterize the relationship of each phosphoproteome, each sample is identified solely by density, treatment and timepoint in figures 2, 3 and 4 respectively. Figure 2 depicts that phosphoproteomes composed of high density (quiescent) cells are shifted right, whereas phosphoproteomes composed of low density (non-quiescent cells) are shifted left, with overlap in the center. This may indicate that there are similarities and slight differences in the composition of phosphoproteomes of quiescent cells and non-quiescent cells, based on the component of this plot. Figure 3 compares the phosphoproteomes by treatment. The majority of the phosphoproteomes of untreated samples lie towards the upper and lower right of the plot, and the majority of the phosphoproteomes of LCA treated samples are placed in the top and bottom left. This illustrates that the phosphoproteomes

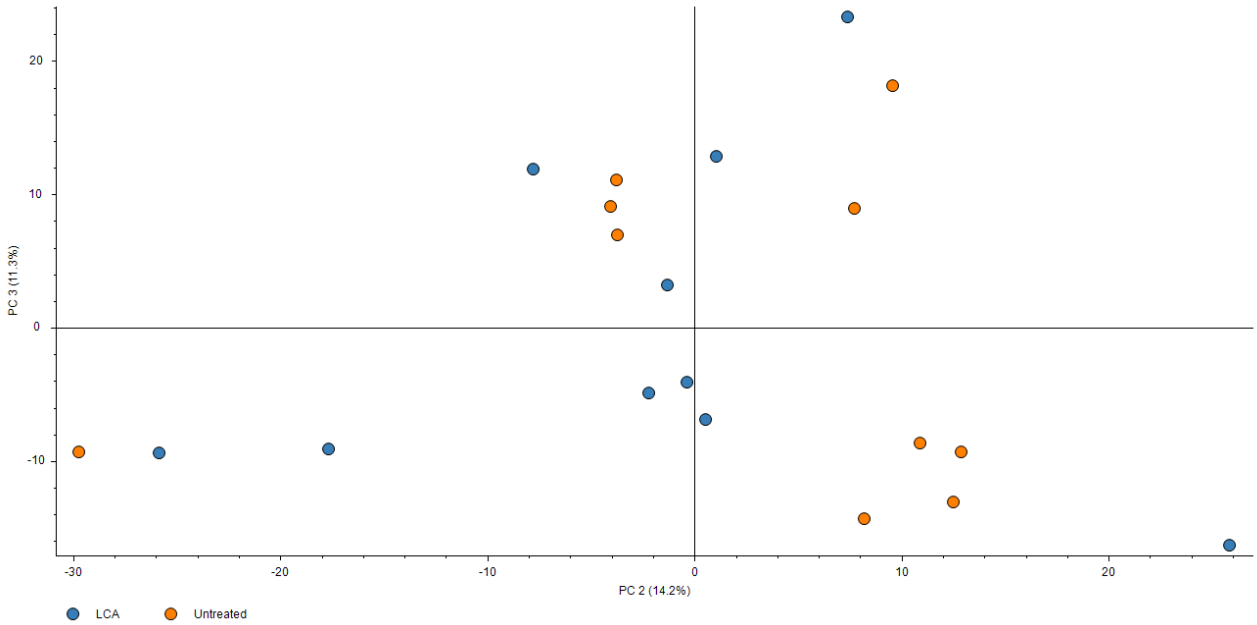


Figure 2. Graph of the principal component analysis of phosphorylated proteins found in high density and low density yeast cells treated with LCA or remained untreated and taken on different days of culturing identified by density.

are similar in LCA treated samples of high and low density across different days, as well as untreated samples. Figure 4 shows the differences in phosphoproteomes by time point, showing that phosphoproteomes of samples cultured on the same day are most similar to one another.

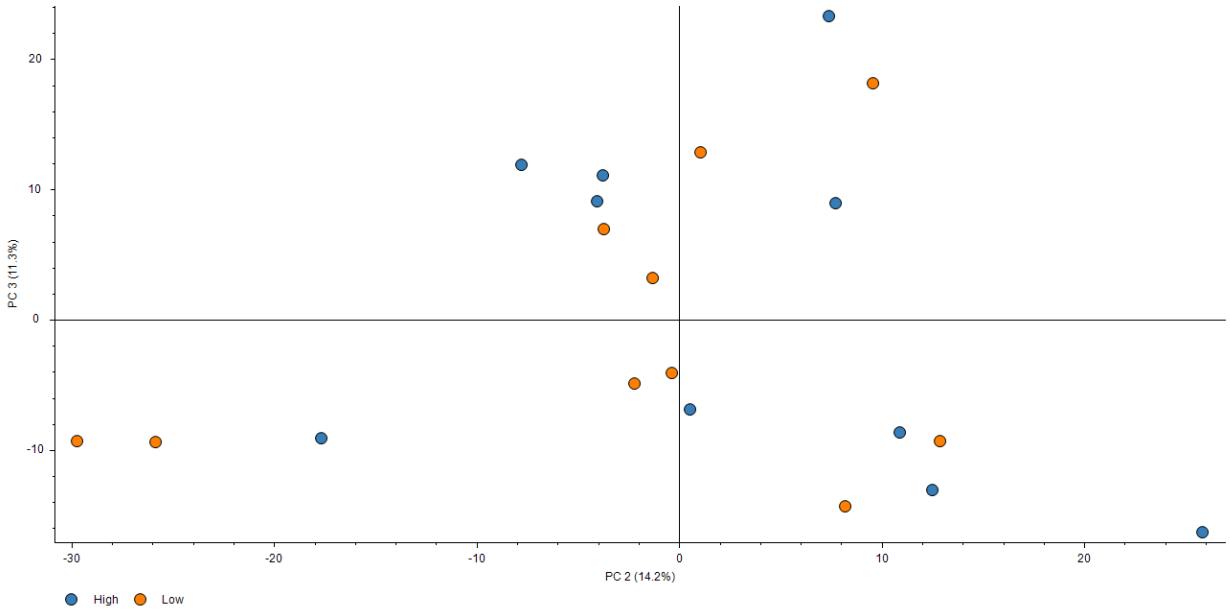


Figure 3. Graph of the principal component analysis of phosphorylated proteins found in high density and low density yeast cells treated with LCA or remained untreated and taken on different days of culturing identified by treatment.

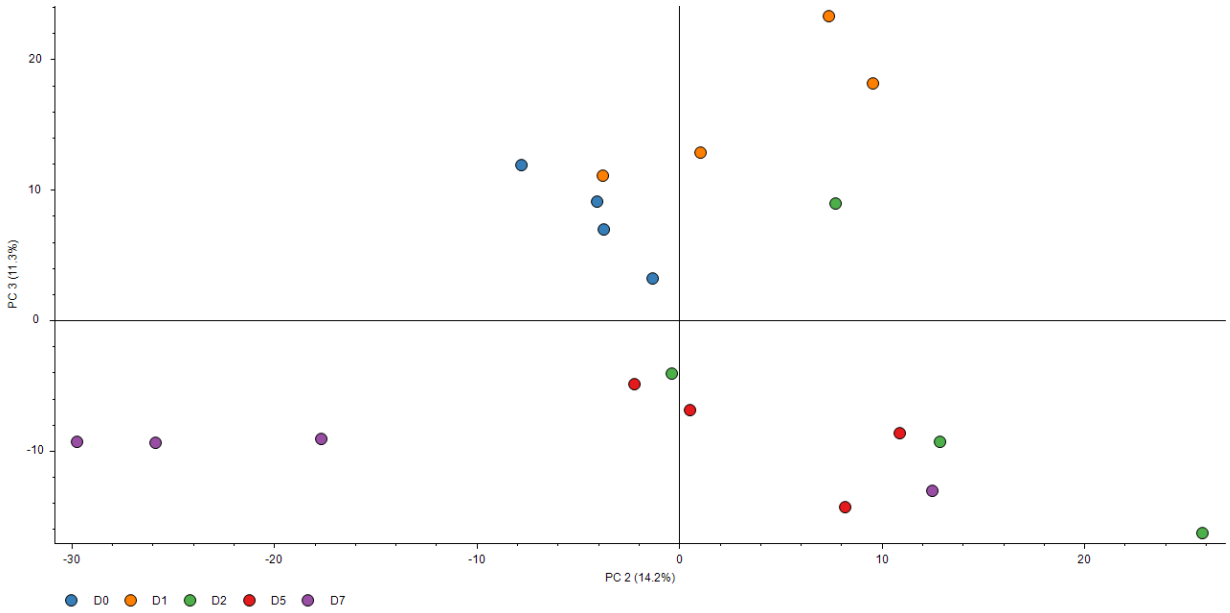


Figure 4. Graph of the principal component analysis of phosphorylated proteins found in high density and low density yeast cells treated with LCA or remained untreated and taken on different days of culturing identified by timepoint.

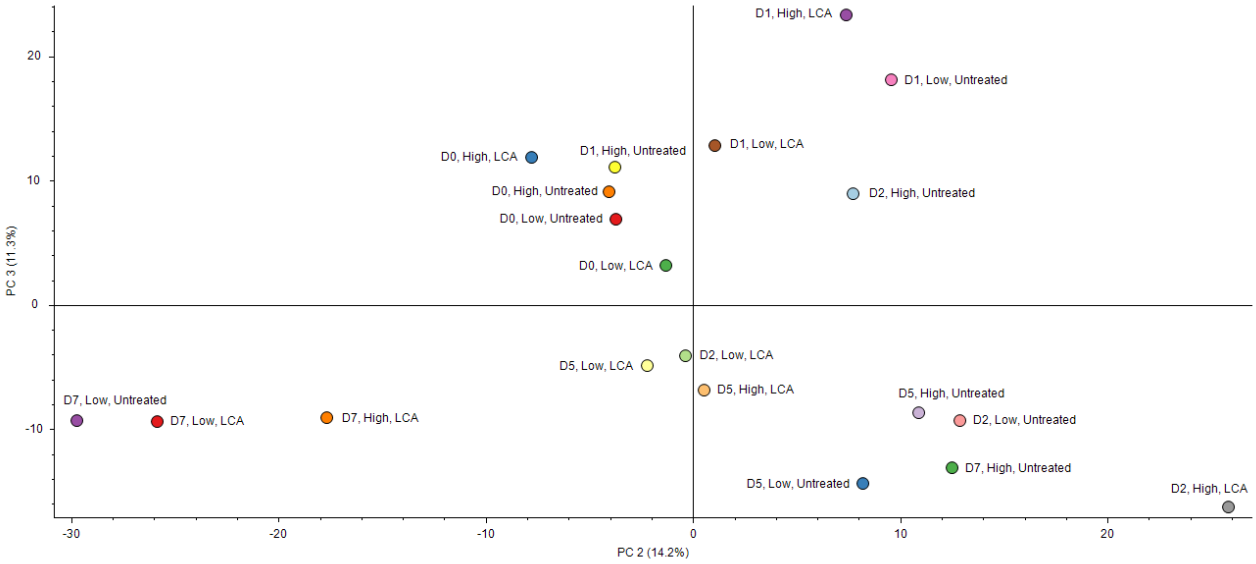


Figure 5. Graph of the principal component analysis of phosphorylated proteins found in high density and low density yeast cells treated with LCA or remained untreated and taken on different days of culturing.

3.3 Cellular localization of phosphorylated proteins

Another way of characterizing a phosphoproteome is by observing the location of the phosphorylated proteins within a cell. Figures 3.1-3.5 display the cellular localizations phosphorylated proteins in high density and low density yeast cells that are either untreated or treated with LCA on different days. Across all 5 timepoints, the abundance of phosphorylated proteins is found principally in the cytoplasm, followed by the nucleus, cell membrane, mitochondrion and endoplasmic reticulum. Signalling networks are often not limited to one location, but rather connect different areas of the cell for constant communication. External factors act as go signals which elicit cascades of phosphorylation events in these networks. High and low density cells treated with LCA show more phosphorylated proteins in the mitochondrion and the endoplasmic reticulum compared to untreated cells, however the difference is not significantly large. LCA is known to induce stress-related pathways in both mitochondrion and endoplasmic reticulum, which may account for this slight variance.

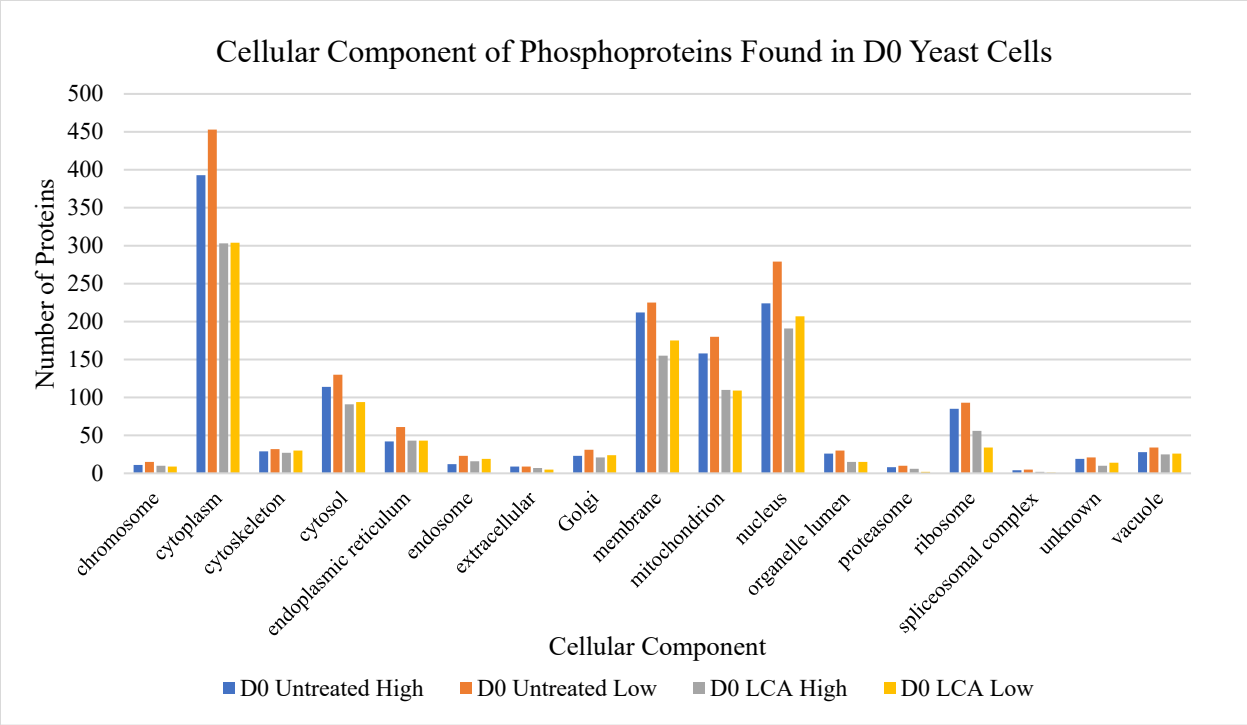


Figure 3.1 Graph with the data on the cellular localization of phosphorylated proteins found in Q and NQ yeast cells treated with LCA or remained untreated and taken on day 0.

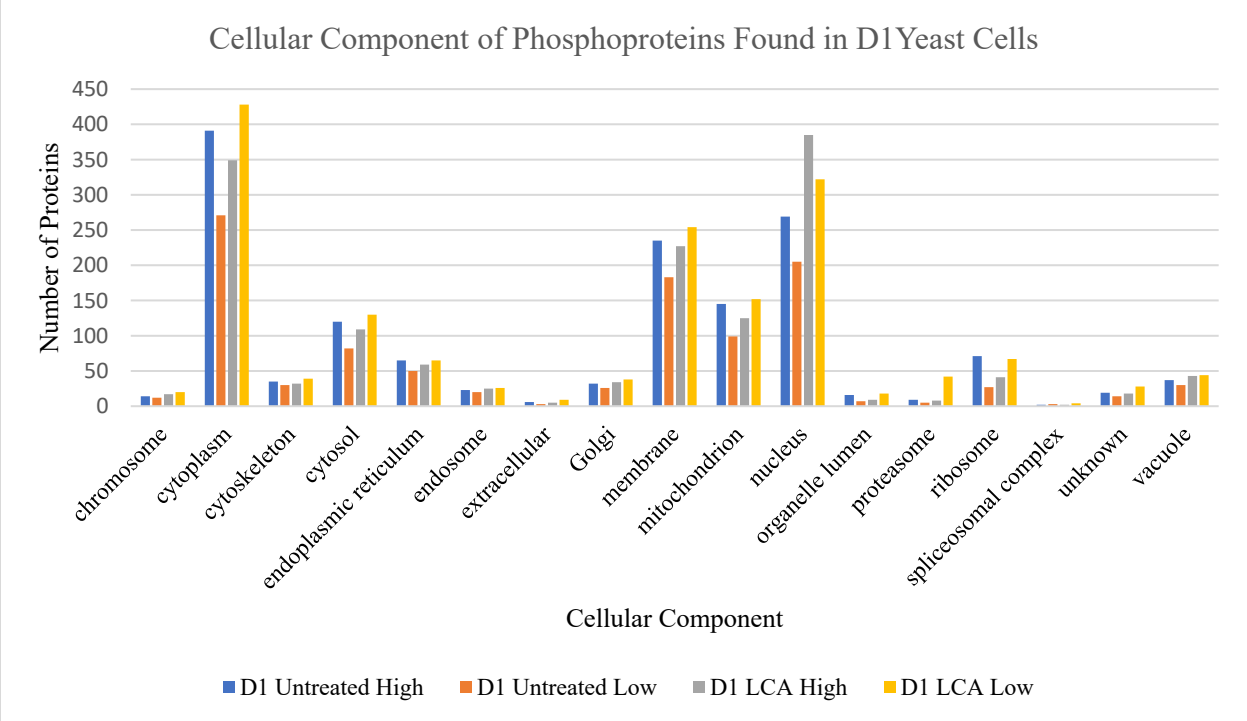


Figure 3.2 Graph with the data on the cellular localization of phosphorylated proteins found in Q and NQ yeast cells treated with LCA or remained untreated and taken on day 1.

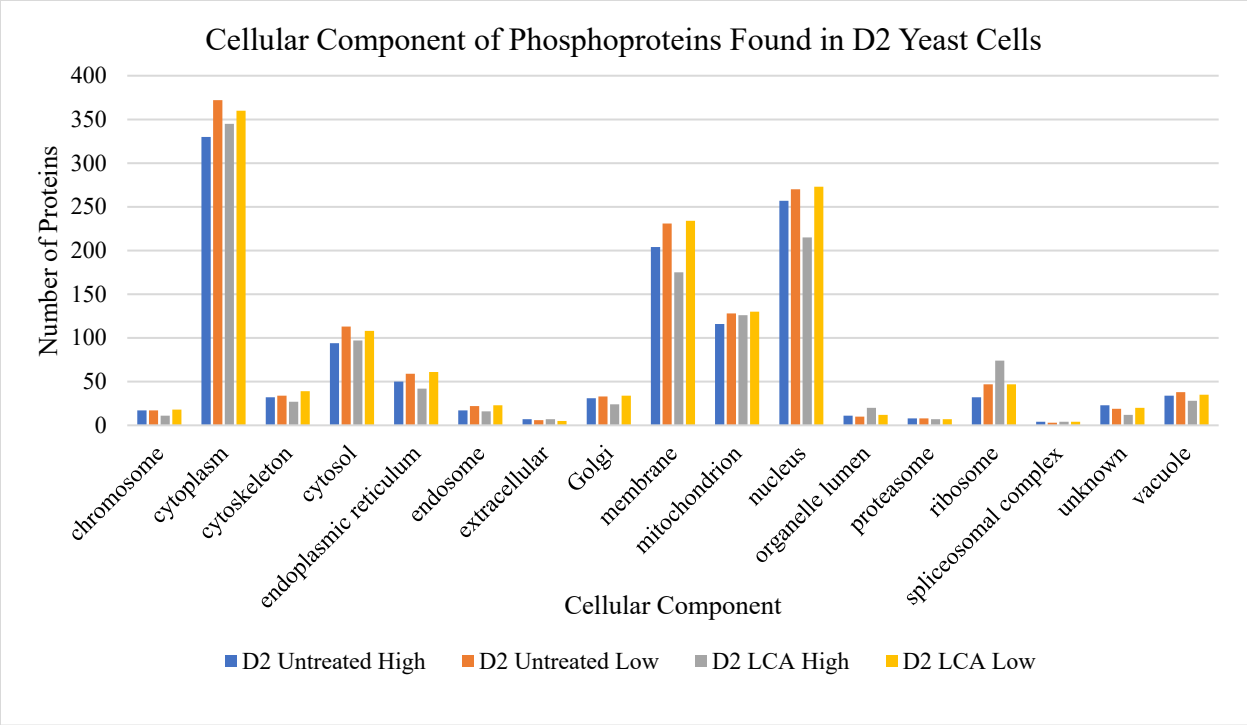


Figure 3.3 Graph with the data on the cellular localization of phosphorylated proteins found in Q and NQ yeast cells treated with LCA or remained untreated and taken on day 2.

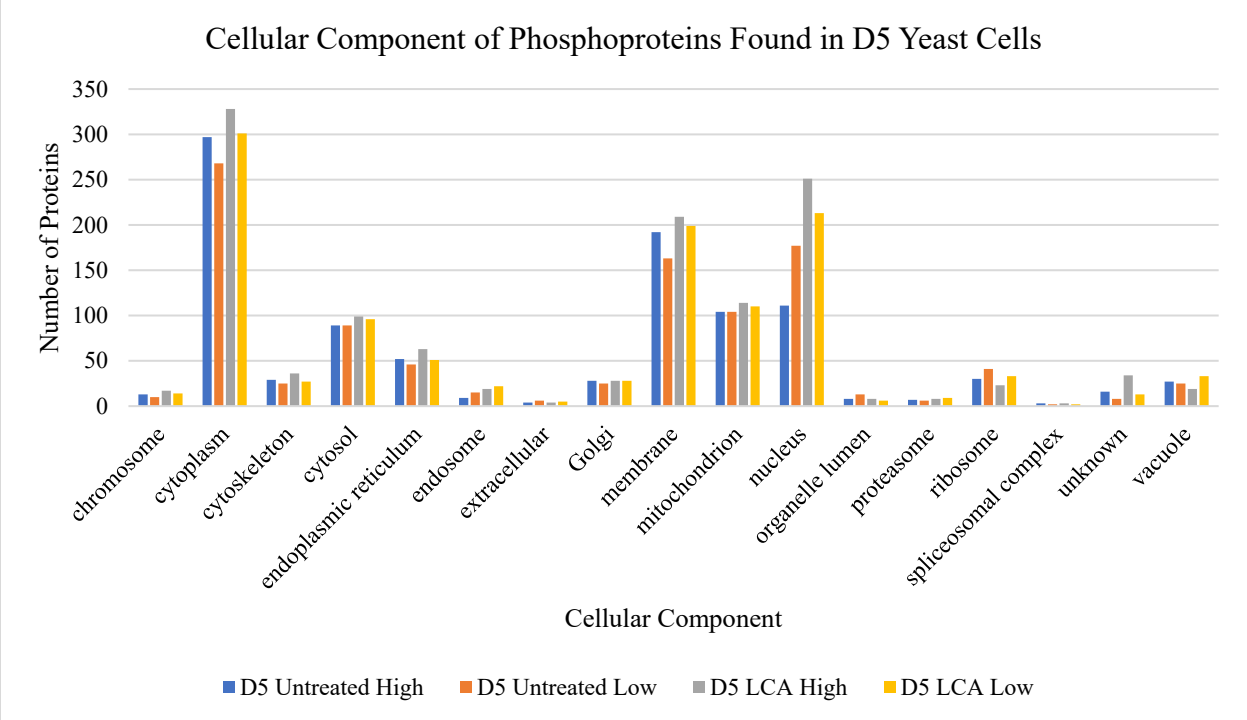


Figure 3.4 Graph with the data on the cellular localization of phosphorylated proteins found in Q and NQ yeast cells treated with LCA or remained untreated and taken on day 5.

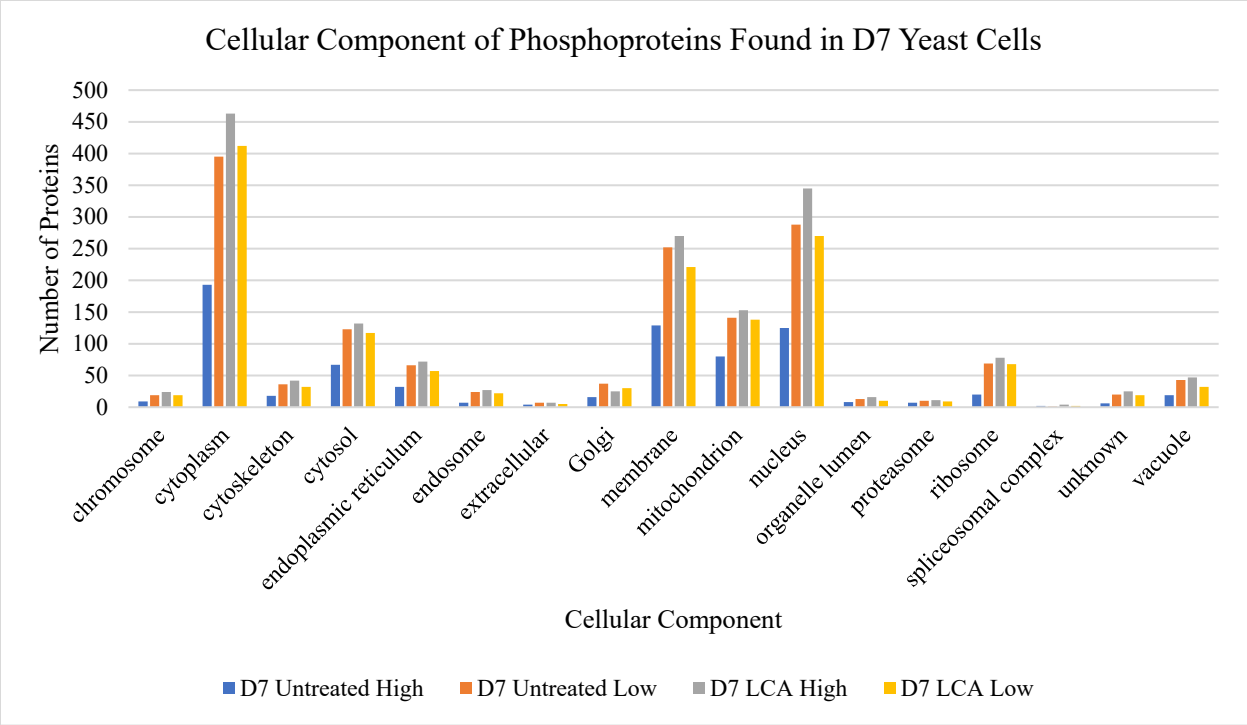


Figure 3.5 Graph with the data on the cellular localization of phosphorylated proteins found in Q and NQ yeast cells treated with LCA or remained untreated and taken on day 7.

3.4 Novel phosphorylation sites and phosphorylated proteins and their known kinases and phosphatases

Mass spectrometry based phosphoproteomics is a valuable tool in the identification of phosphorylation sites and phosphorylated proteins. Table 3.1 outlines the total number of phosphorylation sites discovered by the use of mass spectrometry and Table 3.2 presents each phosphorylation site and their related protein. In total, 832 novel phosphorylation sites were discovered on 373 different proteins. Table 3.3-3.7 itemizes the proteins that were found to be phosphorylated and the known kinases and phosphatases that phosphorylate and dephosphorylate them of high- and low-density cells treated with LCA on different days.

In samples treated with LCA, the most abundant phosphatase known to dephosphorylate the phosphosites discovered were SIT4, PPH22 and CMP2 across all 5 timepoints in high and low density cells. When unsuppressed, SIT4 has key roles in the progression of the cell cycle, and responds to nutrient availability via TORC1 (Woodacre et al. 2013). The function of PPH22 and it's homologue PPH21 are still unknown, however studies including these proteins have shown that in yeast the activation a mutation in PPH22 leads to abnormal cell structure (Ronne et al. 1991). CMP2 is a part of the protein kinase family that is activated by calcium and calmodium. Calcium (Ca^{2+}) is known to be a key messenger molecule in signalling pathways and is also important for the growth and proliferation of cancer cells (Brzozowski and Skelding 2019).

In samples treated with LCA, the most abundant kinases known to phosphorylate the phosphosites discovered were CDC28, MCK1, MEC1 and CLB2 across all 5 timepoints in high- and low-density cells. Other prominent kinases include TOR1, SNF1 and RAD53. CDC is important for cell cycle regulation, while MCK1 is active in the cell in response to stress and activates the calcineurin signalling pathway, which is dependent on calmodulin (Park et al. 2020). MEC1 is the initiator of the DNA damage pathway which induces checkpoint responses in cell cycle arrest (Lanz et al. 2018). CLB2 is also a protein that is involved in the cell cycle, particularly in aiding in the transition from G2 to M (Maher et al. 1995). It is known that LCA causes mild cytotoxicity within cells, therefore the abundance of proteins to combat cell damage and regulate the cell cycle is plausible.

Phosphosites Discovered in Experiment 1	**Phosphosites Discovered in Experiment 2**	**Phosphosites Discovered in Both Experiments**	**Phosphosites Shared by Both Experiments**	**Discovered Phosphosites**
603	697	1300	468	832

Table 3.1 Total number of phosphorylation sites discovered by mass-spectrometry in high- and low-density cells treated with or without LCA on different days of culturing.

Conclusion

In summary, I have found that in response to LCA treatment, the phosphoproteome changes in the following patterns. First, the number of phosphorylated proteins increases in quiescent yeast cell populations in comparison to non-quiescent cells treated with LCA and untreated quiescent cells. Second, phosphoproteomes of similar treatments are share commonality and LCA also increases the amount of phosphorylated proteins in the cytoplasm, nucleus, mitochondria and endoplasmic reticulum across different days of culturing in both quiescent and non-quiescent cells. Through the use of mass spectrometry based phosphoproteomics, I have discovered 832 novel phosphorylation sites and observed kinases such as CDC28, MCK1 and CLB3, which are known to be involved in signalling pathways and cell regulation and phosphatases such as SIT4, PPH22, CMP2 which are involved in the regulation of the cell cycle. Mass spectrometry-based proteomics has elevated our knowledge of the mechanisms that control cellular growth and aging, and still there are many details within this intricate tapestry to be revealed. With the rise of global diseases, combining the study of secondary compounds and signalling networks opens up possibilities for the development of anti-aging therapies and reveals to us that although aging is inevitable our (cellular) ability to adapt is what allows us to thrive.

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Appendix

Protein	Discovered Phosphosites	Protein	Discovered Phosphosites	Protein	Discovered Phosphosites	Protein	Discovered Phosphosites
AAD10	T14	**GTT3**	S121	**PTC3**	T373; S375	**TCB1**	S44; S45
ACC1	S5, S9	**GYP1**	S89	**PTK2**	S63, S73, T729	**TCB3**	T1364
ACK1	S161	**HBT1**	T45; S427; Y428; S431; S795; S850; S932; T939; T940; S941; Y942; S943; Y1003	**PTM1**	S511	**TDA1**	T550
ACM1	T183	**HCA4**	T109; T122; T134	**PUP1**	T47; S49; T50	**TDA3**	S163
ACS1	S2; S4; S67; S628; S629	**HEK2**	S252	**PWP1**	S63	**TDH1**	T151, T152
ADE6	S483; S494; S495	**HPC2**	S223	**PXA1**	S619	**TDH2**	T151; T152
ADH1	S288	**HRR25**	S325; T326; T332	**PXA2**	S632	**TFG1**	S665, T666, T679
ADH2	S2	**HSP26**	S2, S5, T48	**PYC1**	S512	**TGL5**	S654
ADY2	S2; T7; S8; T11; Y20; Y21; S22; S23; S38; S41; Y46	**HSP42**	T236	**PYK2**	T374; T378; S379; T380	**THP3**	T159; T160
AIM3	Y853	**HTS1**	T180; T199; S200	**RBD2**	S255; T257	**TIF1; TIF2**	S11
ALY2	S740, S741	**HXK1**	T156, Y159	**RCN2**	T248; S250; T259	**TIF4631**	S191; S194; S195; S232; T241
AMD1	S66	**HXT5**	S19; T20; S22; S24; Y25; Y40; S51; Y53	**REB1**	T348	**TIP20**	T114
AMD2	S160	**IKI3**	S719; S723	**REG1**	Y497	**TOF1**	S849; T852
AMS1	S2; S3	**IME2**	T33; S35; S48	**RET2**	S235, S271, S275	**TOP2**	S2, T3
APA1	T75	**IML1**	T728	**RFC1**	S88	**TPI1**	T219
APJ1	S96; S97; S105; S110	**IRE1**	S604; S618	**ROM1**	S105	**TPK1**	S43, Y234, T245
APL6	S392	**IST2**	T712	**RPG1**	S504; T940	**TPK3**	T22; Y235; T240; Y241; T242; T246
ARG3	Y318	**JEN1**	S2; S3	**RPL17A**	S141; S142	**TPS3**	Y61; S154
ARP4	T352	**KCS1**	S473	**RPL23B**	S42; S44	**TRM7**	S69
ARP8	T67	**KEL1**	S691; Y700; S742; T755	**RPL27A**	T98; T100	**TRS120**	S221; S223; S224; S225; S226
ASF2	S264	**KEX1**	S666; S673	**RPN11**	T241	**TRS85**	S95; T96
ATG11	S547; S607	**KIN1**	S937; S938	**RPO31**	T1087; T1102	**TSA1**	T167; T179; T183; S187

ATG21	S187	**KOG1**	T474	**RPS11B**	S2; T3	**TSA2**	T174
ATG34	S352; S355; T358	**KRE5**	T595	**RPS14B**	S12; T120	**TSL1**	S85; S86; T87; T88; S137; S138; S186; T205; T215; T219; S220
ATO2	S8; T11; S37	**LAC1**	S7; S9	**RPS21A**	S65	**TUB2**	Y242
BBC1	S77, S83, T810; S815; T818; T820; S822; T824; T835	**LRG1**	T347; T349; S352; S355	**RPS23A**	S128	**UBA2**	S555; S557
BBP1	S69	**LSB3**	T298; S300; S303; S311; S397; S399; T400; S401; S402	**RPS31**	T125	**UBP2**	T912; T1142
BEM3	T458; S460	**LSB5**	Y315	**RRI1**	S378; T379	**UBP3**	S399
BET5	S25; S27; S29	**LSB6**	S319; S320	**RRM3**	S30; Y33	**UBX7**	S347; S348; S352
BMH1	T234	**MAK11**	S376; S380	**RRP15**	S247	**UIP4**	S98; T127
BMH2	S2; T4	**MAM3**	T477; T485; T575	**RSC3**	T241	**UME6**	T403
BNI5	T280	**MCM2**	T547	**RSC6**	T303	**UTP13**	S11
BOP2	S281	**MCM6**	S2; S12	**RSP5**	S140; S141; S161	**UTP20**	S2078; T2088
BUD4	S949; S951; S955	**MDG1**	T180; T181; T256; S257; S272	**RTF1**	Y86	**UTP23**	S217
BUG1	S2; T275	**MDH2**	S4; S8; S13	**RTG2**	T9	**UTR1**	Y104; S451
BUR2	T20; S21	**MDS3**	S671; S1166; T1168	**RTN1**	T233	**VAC8**	S12
CAB3	S241	**MED2**	T171; T172	**RTN2**	T226; S227; S229; S242; S246	**VHS3**	T183
CAB4	S292; S293; S295	**MHP1**	T191; S195; Y204	**RTT10**	T978; T979; S997	**VID28**	S222; S229
CDC19	S377; T378	**MNN2**	T462; S464	**SAF1**	S268	**VPS13**	T438
CDC60	T152	**MOT2**	S364; T379; T382	**SAP1**	T429; T433	**VPS21**	S188
CDS1	S42	**MRPL4**	S287	**SAS10**	S339	**VPS28**	Y152; T162
CHS5	S321;T348; S399; S400; S600	**MSC3**	Y357	**SCD5**	T568	**VTC2**	T180; S189
CLA4	Y812; S815; T816	**MSH4**	T731	**SCP160**	T14, T31	**VTH1**	Y1091
CMK1	S11	**MTC5**	S986, S987	**SDS23**	S61, T410	**WSC3**	S295; S296; S297
CMP2	T23	**MTF2**	T368	**SDS24**	T90; S404; T441	**WTM1**	S8; S12; T13; Y14; S18; S19

COG3	T643	**MUM2**	Y323	**SDS3**	T45; S53	**YAT1**	S389; S390; S391; S392
COG8	T477; T502; T965	**MYO1**	Y1861; S1866; S1873	**SEA4**	S92, S894	**YAT2**	S752, S785. T811, S827
COS9	Y393	**MYO3**	S302; S357	**SEC15**	S200	**YBR225W**	S111; S115; S116
CPR1	S147	**MYO5**	T1036; S1040; T1048; T1051	**SEC2**	S632; S740	**YBR284W**	Y550; T559
CRH1	S24; S30; S35	**NCL1**	T415; T673; S676; T677	**SEC21**	T633; T634	**YCK1**	S236; T238; T491
CRN1	T600	**NGG1**	S141	**SEC27**	S828	**YCK2**	S243; T245
CRP1	T167; T188; S265; T268; T302; T313; S319; S390; S394; T438; S440	**NGL3**	S10; S16; S17; S18; T19	**SEC4**	S206	**YCK3**	T216; Y501
CSR2	S1007	**NHX1**	T565; T568	**SEC6**	T288	**YDL124W**	S2
CTA1	S25; T26	**NIP1**	S222; T228; T239	**SEC7**	S439, T1722, S1723	**YDL199C**	S664; S674; S680
CTF3	T13	**NNF2**	Y508; T520	**SEC8**	T332	**YDL218W**	S272; Y279; S280; T281; S284; S288; Y289; T294; S299; S303; S305; T306
CUE4	T32	**NNK1**	T384	**SFB3**	Y38; S43; T48	**YDR061W**	S282
CUE5	S45	**NOP58**	S444	**SFL1**	T15; T21	**YDR186C; SND1**	T680
CWC22	S30; S40	**NOT3**	S316, S798	**SGM1**	S470	**YDR365W-B**	S3; S7; S10; S13; S20; S365; S406; S409; S411; T412; S416; S418
CYR1	S346, T350	**NSR1**	S143	**SHM1**	T210; S211	**YEL068C**	T19; S33
DBP1	S12	**NTC20**	S42; T49	**SIP4**	S691	**YEN1**	S632
DBP6	T25	**NTH2**	S116	**SIS1**	T181	**YER079W**	T31, T201
DIG1	S37	**NUP1**	S796	**SIS2**	T119; S121; S130; S132	**YER137C-A**	S7; S10; S409
DNM1	S86	**NUP170**	S386; S392; S399	**SLX8**	S92	**YGR054W**	S473, T586
DOT1	T217; S224	**NVJ1**	S182; T187; S188	**SMT3**	T22	**YGR130C**	T337; S228; T339; T342
ECM21	S962, S1027	**ORM2**	T5	**SNA2**	Y75	**YHR097C**	S233

ECM30	S831; T833	**OSH2**	T494; T720	**SOD1**	T29, T30, S32, Y33	**YIL055C**	T365; S555; S565
EIS1	Y704; T706; T759; S780; S781; S795	**PAF1**	T425	**SPC29**	S216	**YKL050C**	S460; T699; S729; S731; S758; T760; S763; T774; S775; S912
EMW1	S613	**PAH1**	T163; S166	**SPO71**	T272	**YKL075C**	S159
ENP2	S671, S672	**PBI2**	T74	**SPO77**	S440; T442; S443; S444	**YKL107W**	S302
ENT2	S175; Y176	**PCK1**	S2; S4; T9; S12; T13; S14; S329; S330; T332; T335	**SPT16**	T463	**YKL133C**	S439
ENT3	S148	**PCL6**	T20	**SPT2**	S191	**YKR018C**	T184; S185; S187; T199
FAB1	S1710; S1712	**PCL9**	S221	**SPT7**	T372	**YLR256W-A**	S409; S411; T412; S416
FAS1	S1113; S1118; S1119	**PCM1**	Y59	**SPT8**	T83, T87	**YLR257W**	T142
FAT3; YKL187C	T705; T716	**PDR18**	S752; T759; S767	**SQS1**	Y103, T107	**YML053C**	S20; S28
FBA1	T39	**PDR8**	T405	**SRB6**	T52; T53; T62	**YMR045C**	S7; S10
FBP1	T18	**PDS5**	Y1112; S1118	**SRP14**	S67; S70	**YMR124W; EPO1**	Y355; S356
FBP26	T437	**PET10**	S2	**SRV2**	T260; T263; S264; S265; S267; S270; T272	**YMR160W**	S67; S68; T71
FMP45	S217; T218; Y219; S220; Y225; Y228; S242; T243; S246; T249; T256	**PEX13**	Y133	**SSA1**	T416; S422; Y428; S479; T492; S495; T499	**YMR206W**	S77; S168; S229
FOL2	T26	**PEX19**	S301	**SSA2**	S479; S486; T492; S495; T499	**YMR265C**	S280
FPR1	S45	**PEX25**	S11	**SSA3**	T493; S496; T500	**YNL054W-B**	S10
FTH1	T120	**PFK2**	S47, T48	**SSA4**	S496, T500	**YNL095C**	S118; S127
FUN19	S267; S269	**PFK26**	S673, S674	**STB2**	T355; S366	**YNL194C**	T230; S233; T235; T237; T241
FUN26	T496; Y506	**PGI1**	S542; T543	**STE20**	T216; T408; T411; T413	**YNL195C**	Y11; S13

GAT1	S373	**PGM1**	T111; S513	**STI1**	T230; S232	**YOL036W**	T273; T279
GCD1	T36	**PGM2**	S512	**SUI3**	S122	**YOL073C; DSC2**	T291; T295
GDS1	S160; S164; Y170	**PIK1**	S601, S603	**SUR7**	S259; S267; T273; S293; S301	**YOR146W**	S6
GID7	T18; S22; S442; S445; S446	**PLB1**	S626; S628; S629	**SWC3**	S9; S12	**YOR389W**	T540; S543
GLG1	S480; S481; S483; S500	**PMD1**	S1413	**SWH1**	T443; S732	**YPL247C**	S345; S346
GLO3	S164	**PNS1**	S25; S63	**SYH1**	T317; T318; S319; S327	**YPL260W; CUB1**	S160
GLT1	S945; S947; S952; T953; S965	**POX1**	S40; S41	**SYO1**	S23	**YPL283W-A; YML133W-A; YER190C-A; YGR296C-A; YNL339W-A**	S154; S161
GNT1	Y387	**PPZ2**	T298; S314; S315; S359	**SYP1**	T433, T443, T445, S561, T571, S574	**YPR172W**	T105
GPA2	T13; T16; S23	**PRS5**	S153, S168, T171	**TAF13**	Y111	**YRB2**	T117, T124, S128
GPI18	S135	**PSK1**	T37	**TAF4**	S9	**ZRC1**	S403; T417; T422; S425

Table 3.2 Novel phosphorylation sites discovered by mass-spectrometry based phosphoproteomics and their related protein in high and low density cells treated with or without LCA at different days of culturing.

Gene Symbol	Description (SGD)	PhosphoSite in Sample	PhosphoSite in Literature	Known Kinases	Predicted Kinases	Known Phosphatases	Reference (BioGrid & iPTMnet)
CDC19	Pyruvate kinase; functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; regulated via allosteric activation by fructose bisphosphate; CDC19 has a paralog, PYK2, that arose from the whole genome duplication	T372; T376; S377; T378	S22	TPK1			7, 104, 122, 142, 217, 317, 370, 374, 379
			T407	CDC28			7, 142, 379
GPM1	Tetrameric phosphoglycerate mutase; mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis	S116	S116	CTK1			7, 32, 56, 122, 139, 142, 217, 370, 374, 379
RAS2	GTP-binding protein; regulates nitrogen starvation response, sporulation, and filamentous growth; farnesylation and palmitoylation required for activity and localization to plasma membrane; homolog of mammalian Ras proto-oncogenes; RAS2 has a paralog, RAS1, that arose from the whole genome duplication	S225; T226; T227	T240	SNF1			7, 32, 217, 379
HTB1	Histone H2B; core histone protein required for chromatin assembly and chromosome function; nearly identical to HTB2; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates reassembly after DNA replication, transcriptional activation, meiotic DSB formation and H3 methylation		S11	STE20			4, 2005
DPS1	Aspartyl-tRNA synthetase, primarily cytoplasmic; homodimeric enzyme that catalyzes the specific aspartylation of tRNA(Asp); class II aminoacyl tRNA synthetase; binding to its own mRNA may confer autoregulation; shares five highly conserved amino acids with human that when mutated cause leukoencephalopathy	S2; S14; S301	S14			SIT4	7, 32, 370, 379

	characterized by hypomyelination with brain stem and spinal cord involvement and leg spasticity (HBSL)						
HXK2	Hexokinase isoenzyme 2; phosphorylates glucose in cytosol; predominant hexokinase during growth on glucose; represses expression of HXK1, GLK1, induces expression of its own gene; antiapoptotic; phosphorylation/dephosphorylation at Ser14 by kinase Snf1p, phosphatase Glc7p-Reg1p regulates nucleocytoplasmic shuttling of Hxk2p; functions downstream of Sit4p in control of cell cycle, mitochondrial function, oxidative stress resistance, chronological lifespan; has paralog HXK1	S15; S158	S15	TPK1		GLC7, REG1	-1, 10, 11, 29, 32, 100, 117, 122, 138, 139, 142, 152, 179, 190, 324, 374
HTA1	Histone H2A; core histone protein required for chromatin assembly and chromosome function; one of two nearly identical subtypes (see also HTA2); DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p; N-terminally propionylated in vivo	S129	S129	MEC1			52, 85, 100, 116, 134, 183, 379, 404, 409, 435
NOT3	Component of the CCR4-NOT core complex, involved in mRNA decapping; involved in transcription initiation and elongation and in mRNA degradation; conserved lysine in human homolog of Not3p and Not5p is mutated in cancers	S304; S316; T319; S324; S325; S326; S344; S347; S348; S441; S442; S446; S450; T454; S798	S450	PHO85	RIM11		7, 32, 100, 116, 139, 142, 152, 217, 373, 374, 379
			T454	PHO85			7, 32, 100, 116, 142, 152, 217, 373, 374, 379
DED1	ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase; required for translation initiation of all yeast mRNAs; binds to mRNA cap-associated factors, and binding stimulates Ded1p RNA-dependent ATPase		S535	MCK1		SIT4	7, 32, 56, 139, 142, 152, 217, 374, 379

	activity; mutation in human homolog DBY is associated with male infertility; human homolog DDX3X complements ded1 null mutation; DED1 has a paralog, DBP1, that arose from the whole genome duplication						
			S539	MCK1		SIT4	7, 32, 56, 142, 152, 217, 374, 379
			S541	MCK1			7, 32, 142, 152, 370, 379
			S543	MCK1			7, 32, 56, 142, 152, 379
			S576	MCK1			32, 56, 142, 152, 217, 379
GPH1	Glycogen phosphorylase required for the mobilization of glycogen; non-essential; regulated by cyclic AMP-mediated phosphorylation; phosphorylation by Cdc28p may coordinately regulate carbohydrate metabolism and the cell cycle; expression is regulated by stress-response elements and by the HOG MAP kinase pathway	T31	T9	TPK1			122, 222, 374
			T27	TPK1			7, 32, 122, 139, 142, 154, 217, 222, 326, 370, 374
			T31	TPK1	CLA4		7, 32, 122, 139, 142, 154, 213, 217, 325, 326, 370, 374, 379
SNF1	AMP-activated S/T protein kinase; forms a complex with Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for	T210; T408; S413	T210	ELM1		GLC7, REG1	7, 37, 92, 142, 143, 237, 250,

	transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis; regulates nucleocytoplasmic shuttling of Hxk2p; regulates filamentous growth and acts as a non-canonical GEF, activating Arf3p during invasive growth; SUMOylation by Mms21p inhibits its function and targets Snf1p for destruction via the Slx5-Slx8 Ub ligase						251, 260, 264, 284, 379, 383
SPT2	Protein involved in negative regulation of transcription; required for RNA polyadenylation; exhibits regulated interactions with both histones and SWI-SNF components; relocalizes to the cytosol in response to hypoxia; similar to mammalian HMG1 proteins	S191; S193	S173	CDC28			7, 32, 116, 142, 370, 373, 379
BCY1	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA); PKA is a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation	S68; S70; S74; S77; S79; T129; S130; T131; T144; S145; S147; T150	S70	MCK1			7, 32, 142, 374, 379
			S89	CDC28			142
			S130	KNS1			7, 32, 142, 217, 370, 374
			S147	KIN4			32, 142, 374
			T129	KNS1			7, 32, 142, 217, 370, 374, 379
			T131	KNS1			7, 32, 142, 217, 370, 374, 379
			T144			CNA1	7, 32, 37, 40, 56, 142, 217, 374
CHO1	Phosphatidylserine synthase; functions in phospholipid biosynthesis; catalyzes the reaction CDP-diaclyglycerol + L-serine = CMP + L-1-phosphatidylserine,	S34; T40; S46; S47; S50; T53; T54	S46	TPK1	TPK1		7, 32, 59, 122, 139, 142, 152,

	transcriptionally repressed by myo-inositol and choline					217, 370, 374, 379
			S47	TPK1		7, 32, 59, 122, 142, 152, 217, 370, 374, 379
FBP1	Fructose-1,6-bisphosphatase; key regulatory enzyme in the gluconeogenesis pathway, required for glucose metabolism; undergoes either proteasome-mediated or autophagy-mediated degradation depending on growth conditions; glucose starvation results in redistribution to the periplasm; interacts with Vid30p	S12; T13; T18	S12	TPK1		126, 142, 247, 332, 333
RPS6A; RPS6B	Protein component of the small (40S) ribosomal subunit; homologous to mammalian ribosomal protein S6, no bacterial homolog; phosphorylated on S233 by Ypk3p in a TORC1-dependent manner, and on S232 in a TORC1/2-dependent manner by Ypk1/2/3p; RPS6B has a paralog, RPS6A, that arose from the whole genome duplication		S232	YPK3		7, 32, 100, 116, 122, 142, 152, 162, 373, 379
SEC7	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors; involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles	S2; T334; S434; S437; S439; S809; T1722; S1723; S1726; S1804	S780	VPS34		7, 32, 142, 217, 374, 379
			S782	VPS34		7, 32, 142, 379
			T1240	CDC28	CDC28	139, 142, 217, 374, 379
CAF20	Phosphoprotein of the mRNA cap-binding complex; involved in translational control; repressor of cap-dependent translation initiation; competes with eIF4G for binding to eIF4E	S91; T99; T101; T102; T104; S105; T106; T111	S58	PSK2		342
			S59	PSK2		342

			S78	FRK1		7, 32, 116, 139, 142, 152, 217, 370, 373, 374, 379
			S91	SLT2	CKA2	7, 32, 116, 139, 142, 217, 370, 373, 374, 379, 452
			T102	SLT2		7, 32, 116, 122, 142, 217, 370, 373, 374, 379
KIN1	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; KIN1 has a paralog, KIN2, that arose from the whole genome duplication	S660; S663; S764; S937; S938	S660	SNF1		7, 32, 142, 379
			S663	SNF1		7, 32, 142, 370, 379
KIN2	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; KIN2 has a paralog, KIN1, that arose from the whole genome duplication		S24	CDC28, CLB2		7, 37, 142, 379
			S609	CDC28		7, 37, 142, 217, 379
			S643	CDC28		7, 32, 37, 116, 142, 370, 373, 374, 379
ABF1	DNA binding protein with possible chromatin-reorganizing activity; involved in transcriptional activation, gene silencing, and DNA replication and repair	S467; S720	S193	MEC1, TEL1		7, 32, 142, 370, 379
			S720	CKA1, CKA2,		7, 116, 139, 142, 217,

				CKB1, CKB2	373, 374, 379, 405
YAK1	Serine-threonine protein kinase; component of a glucose-sensing system that inhibits growth in response to glucose availability; upon nutrient deprivation Yak1p phosphorylates Pop2p to regulate mRNA deadenylation, the co-repressor Crf1p to inhibit transcription of ribosomal genes, and the stress-responsive transcription factors Hsf1p and Msn2p; nuclear localization negatively regulated by the Ras/PKA signaling pathway in the presence of glucose	S38; T288; Y530	Y530	YAK1	7, 13, 122, 142, 152, 175, 217, 374, 379
NSP1	FG-nucleoporin component of central core of the nuclear pore complex; also part of the nuclear pore complex (NPC) nuclear basket; contributes directly to nucleocytoplasmic transport and maintenance of the NPC permeability barrier; found in stable complex with Nup82p, Gle2p and two other FG-nucleoporins (Nup159p and Nup116p); also found in stable complex with Nic96p and two other FG-nucleoproteins (Nup49p and Nup57p)		S361	RAD53	7, 370, 379
CYC8	General transcriptional co-repressor; acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters; can form the prion [OCT+]	S421; T426; S429; S741; S768; S815; S817; S943	S780	MEC1, TEL1	7, 370
			S815	KNS1	7, 32, 142, 217, 370, 374, 379
			S819	KNS1	32, 142, 379
ABP1	Actin-binding protein of the cortical actin cytoskeleton; important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; inhibits barbed-end actin filament elongation; phosphorylation within its Proline-Rich Regio, mediated by Cdc28p and Pho85p, protects Abp1p from	T157; S163; T165; S167; S169; S174; T181; S183; S313; S475; S478; S481	S26	PTK2	32

	proteolysis mediated by its own PEST sequences; mammalian homolog of HIP-55 (hematopoietic progenitor kinase 1 [HPK1]-interacting protein of 55 kDa)					
			S169	CDC28, CLB2		7, 32, 56, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S183	CDC28		7, 32, 56, 100, 116, 142, 152, 217, 370, 373, 374, 379
			S313	CDC28		7, 32, 116, 142, 373, 379
			T30	PTK2		32
			T31	PTK2		32
			T165	CDC28, CLB2	PHO85	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			T181	CDC28, CLB2	PHO85	7, 32, 56, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
HSP26	Small heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation; long-lived protein that is preferentially retained in mother cells and forms cytoplasmic foci; oligomer activation	S2; S5; T42; S47; T48; S208; S211	S208	MEC1, TEL1		7, 52, 100, 142, 152, 379

	requires heat-induced conformational change; also has mRNA binding activity						
			S211	MEC1, TEL1			7, 52, 100, 122, 139, 142, 152, 374, 379
VMA2	Subunit B of V1 peripheral membrane domain of vacuolar H+-ATPase; electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the cytoplasm; protein abundance increases in response to DNA replication stress; human homolog ATP6V1B1, implicated in autosomal-recessive distal renal tubular acidosis (RTA) with sensorineural deafness, complements yeast null mutant	T501; S503; S504; S511; S515	S503	SNF1			7, 32, 56, 370, 374
			S511	MEC1, TEL1	CKA2		7, 116, 139, 142, 152, 217, 370, 373, 374, 379
PDA1	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex; catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA; phosphorylated; regulated by glucose; PDH complex is concentrated in spots within the mitochondrial matrix, often near the ERMES complex and near peroxisomes	Y309; S313; S315	S313	PKP1, PKP2	CKA2		7, 32, 56, 100, 110, 122, 139, 142, 152, 217, 258, 331, 370, 374, 379
OM45	Mitochondrial outer membrane protein of unknown function; major constituent of the outer membrane, extending into the intermembrane space; interacts with porin (Por1p) and with Om14p; imported via the presequence pathway involving the TOM and TIM23 complexes, then assembled in the outer membrane by Mim1p; protein abundance increases in response to DNA replication stress	T207	T207		SNF1	PPH22	7, 32, 139, 379

APA1	AP4A phosphorylase; bifunctional diadenosine 5',5'''-P1,P4-tetraphosphate phosphorylase and ADP sulfurylase involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; catalyzes phosphorolysis of dinucleoside oligophosphates, cleaving substrates' alpha/beta-anhydride bond and introducing Pi into the beta-position of the corresponding NDP formed; protein abundance increases under DNA replication stress; APA1 has a paralog, APA2, that arose from the whole genome duplication	T60; T75	T60	KNS1		7, 32, 142, 217, 370, 379
PFK1	Alpha subunit of heterooctameric phosphofructokinase; involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes	S166; S179; S188; S189; S192	S3	MEC1, TEL1	CKA2	7, 52, 139, 379
PFK2	Beta subunit of heterooctameric phosphofructokinase; involved in glycolysis; indispensable for anaerobic growth; activated by fructose-2,6-bisphosphate and AMP; mutation inhibits glucose induction of cell cycle-related genes	S36; S41; S42; S47; T48; S148; T149; T152; S160; S163; S166; S167; S171; Y172; T173; Y177	S166	SNF1		7, 32, 116, 142, 152, 217, 370, 373, 379
			S167	SNF1		7, 32, 116, 142, 152, 217, 370, 373, 379
			S171	SNF1	CKA2	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S652	PKC1		81
			Y172	SNF1		7, 32, 139
CBF1	Basic helix-loop-helix (bHLH) protein; forms homodimer to bind E-box consensus sequence	T138; S140; S149	S45	MEC1, TEL1		7, 52, 116, 142, 152,

	CACGTG present at MET gene promoters and centromere DNA element I (CDEI); affects nucleosome positioning at this motif; associates with other transcription factors such as Met4p and Isw1p to mediate transcriptional activation or repression; associates with kinetochore proteins, required for chromosome segregation; protein abundance increases in response to DNA replication stress				370, 373, 379
			S48	MEC1, TEL1	7, 32, 52, 116, 142, 152, 370, 373, 379
			S155	SSN3	32, 142, 370, 379
			S156	SSN3	7, 32, 142, 217, 370, 379
			T138	SSN3	7, 32, 139, 142, 217, 379
			T154	CTK1	7, 32, 116, 373, 379
PHO81	Cyclin-dependent kinase (CDK) inhibitor; regulates Pho80p-Pho85p and Pcl7p-Pho85p cyclin-CDK complexes in response to phosphate levels; inhibitory activity for Pho80p-Pho85p requires myo-D-inositol heptakisphosphate (IP7) generated by Vip1p; relative distribution to the nucleus increases upon DNA replication stress	S542; S543	S956	RAD53	7, 52
FPR1	Peptidyl-prolyl cis-trans isomerase (PPIase); binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; N-terminally propionylated in vivo; mutation is functionally complemented by human FKBP1A	S45; S46; S51	S51	PSK2	7, 32, 142, 370, 379

MCK1	Dual-specificity ser/thr and tyrosine protein kinase; roles in chromosome segregation, meiotic entry, genome stability, phosphorylation-dependent protein degradation (Rcn1p and Cdc6p), inhibition of protein kinase A, transcriptional regulation, inhibition of RNA pol III, calcium stress and inhibition of Clb2p-Cdc28p after nuclear division; MCK1 has a paralog, YGK3, that arose from the whole genome duplication	S24; S27; T30; S196; S198; Y199; S202	Y199	MCK1		7, 32, 142, 152, 217, 328, 374, 379
SNF2	Catalytic subunit of the SWI/SNF chromatin remodeling complex; involved in transcriptional regulation; contains DNA-stimulated ATPase activity; functions interdependently in transcriptional activation with Snf5p and Snf6p		S1340	RAD53		7, 142, 370, 374
SIN3	Component of both the Rpd3S and Rpd3L histone deacetylase complexes; involved in transcriptional repression and activation of diverse processes, including mating-type switching and meiosis; involved in the maintenance of chromosomal integrity	T303; T304; T308	S316	CDC28		7, 32, 100, 142, 217, 374, 379
			S1126	MEC1, TEL1		52
			T304	CDC28		7, 32, 142, 217, 374, 379
HSP12	Plasma membrane protein involved in maintaining membrane organization; involved in maintaining organization during stress conditions; induced by heat shock, oxidative stress, osmostress, stationary phase, glucose depletion, oleate and alcohol; protein abundance increased in response to DNA replication stress and dietary restriction; regulated by the HOG and Ras-Pka pathways; required for dietary restriction-induced lifespan extension		S21	MEC1, TEL1	PTC6	7, 32, 52, 56, 116, 142, 370, 373, 379
			S24	PKP1	PTC6	7, 32, 56, 116, 142,

						370, 373, 379
			S59	PKP1		7, 32, 116, 142, 370, 373, 379
			S73	PKP1		7, 32, 116, 139, 142, 370, 373, 379
			S87	PKP1		7, 32, 370
			Y25	PKP1		32, 142
SGV1	Cyclin (Bur2p)-dependent protein kinase; part of the BUR kinase complex which functions in transcriptional regulation; phosphorylates the carboxy-terminal domain (CTD) of Rpo21p and the C-terminal repeat domain of Spt5p; recruits Spt6p to the CTD at the onset of transcription; regulated by Cak1p; similar to metazoan CDK9 proteins	S417	T240	CAK1	SNF1	7, 37, 56, 100, 122, 139, 142, 152, 379, 442
GSY1	Glycogen synthase; expression induced by glucose limitation, nitrogen starvation, environmental stress, and entry into stationary phase; GSY1 has a paralog, GSY2, that arose from the whole genome duplication; relocalizes from nucleus to cytoplasmic foci upon DNA replication stress	S651; S655	S651	MCK1	RIM11	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S655	MCK1	PHO85	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
STE11	Signal transducing MEK kinase; involved in pheromone response and pseudohyphal/invasive growth pathways where it phosphorylates Ste7p, and the high osmolarity response pathway, via phosphorylation of Pbs2p; regulated by Ste20p and Ste50p; protein abundance		S281	STE20		86

	increases in response to DNA replication stress					
			S285	STE20		86
			T286	STE20		86
SSD1	Translational repressor with a role in polar growth and wall integrity; regulated by Cbk1p phosphorylation to effect bud-specific translational control and localization of specific mRNAs; interacts with TOR pathway components; contains a functional N-terminal nuclear localization sequence and nucleocytoplasmic shuttling appears to be critical to Ssd1p function	S480; S481; T482; S487; S489; S491; S492; T494	S42	CBK1		156, 217
			S126	CBK1		32, 142, 152, 156
			S152	CBK1		32, 142, 156, 374, 379
			S164	CBK1		32, 56, 142, 156, 217, 370, 374
			S228	CBK1		32, 142, 156
			S231	CDC28		7, 32, 142, 156, 370
			S267	CLB2, CDC28	CDC28	7, 32, 139, 142, 152
			S286	CDC28		7, 32, 142, 152, 156, 374, 379
			S293	CKB1		32, 142, 156
			S319	CKB1		156
			S492	CDC28		7, 32, 100, 116, 142, 217, 370, 373, 374, 379
			T261	CBK1		156
NAP1	Histone chaperone; involved in histone exchange by removing and replacing histone	T20; T24	S159	CKA1, CKA2,		7, 32, 37, 43, 116,

	H2A-H2B dimers or histone variant dimers from assembled nucleosomes; involved in the transport of H2A and H2B histones to the nucleus; required for the regulation of microtubule dynamics during mitosis; interacts with mitotic cyclin Clb2p; controls bud morphogenesis; phosphorylated by CK2; protein abundance increases in response to DNA replication stress			CKB1, CKB2			139, 142, 152, 217, 370, 373
			S177	CKA1, CKA2, CKB1, CKB2	CKA2		7, 32, 37, 43, 116, 139, 142, 152, 217, 370, 373, 379
			S397	CKA1, CKA2, CKB1, CKB2			7, 43
			T20	PTK2			7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
			T24	PTK2			7, 32, 37, 116, 122, 142, 152, 217, 373, 374, 379
HSP30	Negative regulator of the H(+)-ATPase Pma1p; stress-responsive protein; hydrophobic plasma membrane localized; induced by heat shock, ethanol treatment, weak organic acid, glucose limitation, and entry into stationary phase	S308; T331	S308		CDC28	SIT4	7, 32, 100, 139, 142, 370, 379
CDC48	AAA ATPase; subunit of polyUb-selective segregase complex involved in ERAD, INM-associated degradation (INMAD), mitotic spindle disassembly, macroautophagy, PMN,	S770	S770	MPS1			7, 32, 37, 56, 116, 142, 217,

	ribosome-associated degradation, ribophagy, homotypic ER membrane fusion, SCF complex disassembly, cell wall integrity during heat stress, and telomerase regulation; mobilizes membrane-anchored transcription factors by regulated Ub/proteasome-dependent processing (RUP); human ortholog VCP complements a cdc48 mutant					370, 373, 374, 379
			T735	MPS1	CKA2	7, 37, 139, 142, 370, 379
GSY2	Glycogen synthase; expression induced by glucose limitation, nitrogen starvation, heat shock, and stationary phase; activity regulated by cAMP-dependent, Snf1p and Pho85p kinases as well as by the Gac1p-Glc7p phosphatase; GSY2 has a paralog, GSY1, that arose from the whole genome duplication; relocalizes from cytoplasm to plasma membrane upon DNA replication stress	S651; S655	S651	MCK1	RIM11	7, 32, 37, 100, 122, 133, 139, 142, 148, 149, 152, 217, 342, 370, 374, 379, 427
			S655	PCL10, PHO85		7, 26, 37, 100, 122, 133, 142, 148, 149, 217, 342, 370, 374, 379, 427
			T668	PCL10, PHO85		26, 133, 148, 149, 427
MIG1	Transcription factor involved in glucose repression; sequence specific DNA binding protein containing two Cys2His2 zinc finger motifs; regulated by the SNF1 kinase and the GLC7 phosphatase; regulates filamentous growth along with Mig2p in response to glucose depletion; activated in stochastic pulses of nuclear localization, shuttling between cytosol and nucleus depending on	S278	S222	SNF1		32, 77, 142, 152, 367, 428

	external glucose levels and its phosphorylation state					
			S264	CLB2, CDC28		32, 142, 152, 379
			S278	SNF1		7, 32, 77, 142, 152, 299, 367, 379, 396, 428
			S311	SNF1		6, 7, 77, 122, 142, 152, 217, 299, 307, 370, 379, 396, 428
			S381	SNF1		7, 77, 142, 367, 428
FUN19	Non-essential protein of unknown function; expression induced in response to heat stress; FUN19 has a paralog, YOR338W, that arose from the whole genome duplication	T194; S207; S267; S269	S207	CDC28	PHO85	7, 139, 142
			S211	CDC28		7, 142
BMH1	14-3-3 protein, major isoform; controls proteome at post-transcriptional level, binds proteins and DNA, involved in regulation of exocytosis, vesicle transport, Ras/MAPK and rapamycin-sensitive signaling, aggresome formation, spindle position checkpoint; protein increases in abundance and relative distribution to the nucleus increases upon DNA replication stress; antiapoptotic gene similar to human 14-3-3; BMH1 has a paralog, BMH2, that arose from whole genome duplication	T231; T234; S235; S238; S240	S238	HRR25		32, 63, 417
BEM1	Protein containing SH3-domains; involved in establishing cell polarity and morphogenesis; functions as a scaffold protein for complexes that include Cdc24p, Ste5p, Ste20p, and Rsr1p	S458	S72			7, 32, 131, 370, 379, 401

			S458	SNF1		7, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
MCM2	Protein involved in DNA replication; component of the Mcm2-7 hexameric helicase complex that binds chromatin as a part of the pre-replicative complex; relative distribution to the nucleus increases upon DNA replication stress	T547	S107	CDC7		323
			S164	CDC7		39, 142, 310, 311, 323, 376
			S170	CDC7		39, 142, 310, 311, 323, 376
CDC3	Component of the septin ring that is required for cytokinesis; septins are GTP-binding proteins that assemble with other septins into rod-like complexes that can associate with other rods to form filament polymers; septin rings at the mother-bud neck act as scaffolds for recruiting factors needed for cell division and as barriers to prevent diffusion of specific proteins between mother and daughter cells	S2; S9	S498	CTK1		32, 379
			S503	CLB2, CDC28		32, 116, 122, 142, 152, 373, 374, 379, 389
			S509	CLB2, CDC28		7, 32, 37, 116, 142, 152, 217, 373, 374, 379, 389
HOG1	Mitogen-activated protein kinase involved in osmoregulation; controls global reallocation of RNAPII during osmotic shock; mediates	Y176; T179	T174	PBS2	PTC2, PTC3	18, 30, 32, 37, 100, 152, 241,

	recruitment/activation of RNAPII at Hot1p-dependent promoters; binds calmodulin; stimulates antisense transcription to activate CDC28; defines novel S-phase checkpoint with Mrc1p that prevent replication/transcription conflicts; nuclear form represses pseudohyphal growth; autophosphorylates; protein abundance increases under DNA replication stress					352, 379, 408, 420
			Y176	PBS2	PTC1	7, 18, 30, 32, 100, 139, 142, 152, 241, 352, 379, 408, 420
NIP1	eIF3c subunit of the eukaryotic translation initiation factor 3 (eIF3); involved in the assembly of preinitiation complex and start codon selection; eIF3 is also involved in programmed stop codon readthrough	S98; S99; S103; S222; T228; T239	S98	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
			S99	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
			S103	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
NUP2	Nucleoporin involved in nucleocytoplasmic transport; binds to either the nucleoplasmic or cytoplasmic faces of the nuclear pore complex depending on Ran-GTP levels; also has a role in chromatin organization	T14; S17; S20; S84; S203; S205; S537; S538; S540; T577; S581	S17	MCK1		7, 32, 56, 100, 116, 142, 152, 217, 369, 373, 374, 379
			S20	MCK1		7, 32, 56, 100, 116, 142, 152, 217, 369,

						373, 374, 379
			S68	RAD53		7, 139, 142, 370
			S203	RAD53	PTP1	7, 32, 56, 116, 142, 152, 217, 370, 373, 374
			S205	ALK2	PTP1	7, 32, 56, 116, 142, 152, 217, 370, 373, 374
			S248	RAD53		7, 370
			S284	RAD53		7, 370
			S317	RAD53		7, 370
			S351	RAD53		7, 52, 370
			S368	RAD53		7, 142, 370, 379
			S399	MEC1, TEL1		370, 379
			S512	RAD53		370
			S523	RAD53		370
PAN1	Part of actin cytoskeleton-regulatory complex Pan1p-Sla1p-End3p; associates with actin patches on cell cortex; promotes protein-protein interactions essential for endocytosis; binds to and activates Arp2/3 complex in vitro; phosphorylation of Thr-1225 is regulated by MAPK Hog1p in response to osmotic stress; previously thought to be a subunit of poly(A) ribonuclease	T570; T993; S1003; S1250; S1253; S1255; T1256	T148	PRK1		147, 395, 453
			T170	PRK1		147, 395, 453
			T194	PRK1		147, 395, 453
			T221	PRK1		395, 453

			T241	PRK1	7, 147, 395, 453
			T398	PRK1	147, 395, 453
			T415	PRK1	147, 395, 453
			T428	PRK1	147, 395, 453
			T452	PRK1	147, 395, 453
			T473	PRK1	147, 395, 453
			T504	PRK1	147, 395, 453
			T513	PRK1	147, 395, 453
			T544	PRK1	147, 395, 453
			T551	PRK1	147, 395, 453
			T566	PRK1	7, 146
			T570	PRK1	7, 32, 142, 147, 152, 379, 395, 453
SIP1	Alternate beta-subunit of the Snf1p kinase complex; may confer substrate specificity; vacuolar protein containing KIS (Kinase-Interacting Sequence) and ASC (Association with Snf1 kinase Complex) domains involved in protein interactions	S331	S198	CDC28	7, 142, 217, 379
			S200	CDC28	7, 116, 142, 217, 373, 374, 379
YEL043W	Predicted cytoskeleton protein involved in intracellular signaling; based on quantitative analysis of protein-protein interaction maps; may interact with ribosomes, based on co-purification studies; contains fibronectin type III domain fold	S524	S847	CDC28	142

			S862	CDC28			142
SLA1	Cytoskeletal protein binding protein; required for assembly of the cortical actin cytoskeleton; interacts with proteins regulating actin dynamics and proteins required for endocytosis; found in the nucleus and cell cortex; has 3 SH3 domains	S794; T797; S799; T831; T834; T835	S437	CLB2, CDC28			7, 32, 142, 152, 370, 374, 379
			S449			PSR2	7, 32, 116, 142, 217, 373, 379
UGP1	UDP-glucose pyrophosphorylase (UGPase); catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; involved in PKA-mediated oxidative stress resistance and long-term survival in stationary phase; UGP1 has a paralog, YHL012W, that arose from the whole genome duplication		S11	PSK2			7, 32, 37, 56, 100, 116, 122, 142, 217, 342, 368, 373, 374, 379
CBF5	Pseudouridine synthase catalytic subunit of box H/ACA snoRNPs; acts on large and small rRNAs, on snRNA U2, and on some mRNAs; mutations in human ortholog dyskerin cause the disorder dyskeratosis congenita; small nucleolar ribonucleoprotein particles are also known as snoRNPs	T378; S398	S395	MEC1, TEL1	RIM11		7, 32, 52, 116, 139, 142, 373, 374, 379
			S399	MEC1, TEL1			7, 32, 52, 116, 142, 370, 373, 374, 379
			T396	FRK1	CKA2		7, 32, 139, 142
PPZ2	Serine/threonine protein phosphatase Z, isoform of Ppz1p; involved in regulation of potassium transport, which affects osmotic stability, cell cycle progression, and halotolerance	T298; S299; S310; S314; S315; S317; S359; S362	S299	CLB2, CDC28			7, 37, 142, 374, 379

			S310	CLB2, CDC28	7, 37, 116, 142, 373, 374, 379
SLA2	Adaptor protein that links actin to clathrin and endocytosis; involved in membrane cytoskeleton assembly and cell polarization; present in the actin cortical patch of the emerging bud tip; dimer in vivo		S308	CDC28	7, 32, 100, 142, 152, 217, 374, 379
			T290	SSK2	7, 32, 142, 370, 379
			T294	CDC28	7, 32, 142, 217, 370, 374, 379
			T296	CDC28	7, 32, 100, 122, 142, 217, 370, 374, 379
			T298	CDC28	7, 32, 142, 370, 379
PGM1	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; PGM1 has a paralog, PGM2, that arose from the whole genome duplication	T111; T118; S120; S513	S120	FRK1	7, 32, 116, 122, 142, 152, 217, 370, 373, 374, 379
TRM2	tRNA methyltransferase; 5-methylates the uridine residue at position 54 of tRNAs and may also have a role in tRNA stabilization or maturation; endo-exonuclease with a role in DNA repair	S93	S92	KNS1	32, 116, 139, 142, 152, 217, 373, 374, 379
			S93	KNS1	7, 32, 56, 142, 152, 217, 370, 374, 379
TGL1	Steryl ester hydrolase; one of three gene products (Yeh1p, Yeh2p, Tgl1p) responsible for steryl ester hydrolase activity and involved in sterol homeostasis; localized to lipid particle membranes	S462; S466; S538	S466	CDC28	142, 379

			S492	TPK3		7, 32, 142, 370, 374, 379
EDE1	Scaffold protein involved in the formation of early endocytic sites; putative regulator of cytokinesis; homo-oligomerization is required for localization to and organization of endocytic sites; has a network of interactions with other endocytic proteins; binds membranes in a ubiquitin-dependent manner; may also bind ubiquitinated membrane-associated proteins; interacts with Cmk2 and functions upstream of CMK2 in regulating non-apoptotic cell death; homolog of mammalian Eps15	S241; S931; S1006; S1008; S1011; S1012; T1065; S1093; S1095; S1096; S1100; S1104; T1160; T1178; S1179; S1181; S1187; T1307; S1309	S241		PTC4	7, 32, 100, 122, 142, 152, 217, 370, 374, 379
			S244		PTC4	7, 32, 100, 122, 142, 152, 217, 374, 379
			S249		PTC4	7, 32, 142, 152, 217, 374, 379
			S527		PSR2	32, 152, 370
			S1069		CMP2	7, 32, 142, 379
			S1096	FUS3		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			S1100	PHO85		7, 32, 56, 100, 116, 142, 152, 217, 370, 373, 374, 379
			T238	CDC28		7, 142, 217, 379
			T1072		CMP2	7, 32, 142, 379

PIN4	Protein involved in G2/M phase progression and response to DNA damage; interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage	T512; S538; S541; S545; S653; S655	S466	CDC28			7, 32, 116, 122, 139, 142, 217, 373, 374, 379
			S541	CDC28			32, 122, 142, 152, 379
			S653			SIT4	7, 32, 37, 116, 122, 142, 370, 373, 374, 379
			S655			SIT4	7, 32, 116, 122, 142, 370, 373, 374, 379
SHP1	UBX domain-containing substrate adaptor for Cdc48p; ubiquitin regulatory X domain-containing protein that acts as a substrate recruiting cofactor for Cdc48p; positively regulates Glc7p PPase activity to promote growth and mitotic progression in complex with Cdc48p; ubiquitinated protein interactor involved in ER-associated degradation (ERAD); regulated by nuclear Ub-dependent degradation (INMAD pathway) independent of the Asi and Doa10 complexes; homolog of human p47 (NSFL1C)	S97; S106; T107; S115; S224; S315; S321; S322; T331	S106	KNS1			7, 32, 100, 116, 152, 373, 379
			S108	PTK1			7, 32, 100, 116, 152, 370, 373, 379
			S315	CDC28	CDC28		7, 32, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379

			S322	CDC28	7, 32, 139, 142, 217, 374, 379
SCD5	Protein required for normal actin organization and endocytosis; targeting subunit for protein phosphatase type 1; undergoes Crm1p-dependent nuclear-cytoplasmic shuttling; multicopy suppressor of clathrin deficiency	S564; T568	T416	PRK1	146, 454
			T450	PRK1	146, 454
			T490	PRK1	7, 142, 146, 370, 454
TSA1	Thioredoxin peroxidase; acts as both ribosome-associated and free cytoplasmic antioxidant; self-associates to form high-molecular weight chaperone complex under oxidative stress; chaperone activity essential for growth in zinc deficiency; required for telomere length maintenance; binds and modulates Cdc19p activity; protein abundance increases, forms cytoplasmic foci during DNA replication stress; TSA1 has a paralog, TSA2, that arose from the whole genome duplication	T167; T174; T179; T183; S187	T174	FRK1	7, 32, 116, 142, 373, 379
GCS1	ADP-ribosylation factor GTPase activating protein (ARF GAP); involved in ER-Golgi transport; required for prospore membrane formation; regulates phospholipase Spo14p; shares functional similarity with Glo3p; GCS1 has a paralog, SPS18, that arose from the whole genome duplication	S149; T151; S157; T161; S168; T170	S157	CKA1	7, 32, 142, 217, 370, 374, 379
			T151	MCK1	32, 142, 152, 217
			T161	CDC28	7, 32, 142, 217, 370, 374, 379
			T170	CLB2, CDC28	7, 32, 100, 142, 370, 379
DEF1	RNAPII degradation factor; forms a complex with Rad26p in chromatin, enables	T258; S260; S307	S273	RAD53	56, 116, 370

	ubiquitination and proteolysis of RNAPII present in an elongation complex; mutant is deficient in Zip1p loading onto chromosomes during meiosis						
BDF1	Protein involved in transcription initiation; functions at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p; BDF1 has a paralog, BDF2, that arose from the whole genome duplication	S270; S612; S613; S615; T617	S630	MEC1, TEL1			52, 379
SWH1	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats and FFAT motif; interacts with ER anchor Scs2p at the nucleus-vacuole junction; regulated by sterol binding; SWH1 has a paralog, OSH2, that arose from the whole genome duplication	T432; S442; T443; S488; S490; S492; S678; S683; T694; S732; T1053; S1056	S1056	SNF1	SNF1		7, 32, 139, 142, 370, 379
			T1053	SNF1	SNF1		7, 32, 139, 370, 379
SIS2	Negative regulatory subunit of protein phosphatase 1 (Ppz1p); involved in coenzyme A biosynthesis; subunit of phosphopantothenoylcysteine decarboxylase (PPCDC: Cab3p, Sis2p, Vhs3p) complex and the CoA-Synthesizing Protein Complex (CoA-SPC: Cab2p, Cab3p, Cab4p, Cab5p, Sis2p and Vhs3p); SIS2 has a paralog, VHS3, that arose from the whole genome duplication	T119; S121; S124; S130; S132	S47	CDC28			7, 32, 142, 217, 370, 374, 379
			S56	CDC28			7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
EAP1	eIF4E-associated protein, competes with eIF4G for binding to eIF4E; accelerates mRNA degradation by promoting decapping, facilitated by interaction with eIF4E; essential for Puf5p mediated repression; associates	S389; S390; T391	S363			PSR1	32, 142

	with Puf5p and Dhh1p; inhibits cap-dependent translation; functions independently of eIF4E to maintain genetic stability; plays a role in cell growth, implicated in the TOR signaling cascade					
			S387	MCK1		7, 32
YKR018C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; protein abundance increases in response to DNA replication stress; YKR018C has a paralog, IML2, that arose from the whole genome duplication	T184; S185; S187; S192; T193; T196; T199; S246; S375; S377; S380	S380	PKH2		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
GPT2	Glycerol-3-phosphate/dihydroxyacetone phosphate sn-1 acyltransferase; located in lipid particles and the ER; involved in the stepwise acylation of glycerol-3-phosphate and dihydroxyacetone in lipid biosynthesis; the most conserved motifs and functionally relevant residues are oriented towards the ER lumen	S631; S632; S668; S671; T692; S693	T692	YPK1	CKA2	7, 32, 122, 139, 142, 370, 374, 379
PGM2	Phosphoglucomutase; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; functions as the acceptor for a Glc-phosphotransferase; protein abundance increases in response to DNA replication stress; PGM2 has a paralog, PGM1, that arose from the whole genome duplication	T111; T117; S119; S512	S119	RAD53		7, 32, 116, 122, 142, 370, 373, 374, 379
STV1	Subunit a of the vacuolar-ATPase V0 domain; one of two isoforms (Stv1p and Vph1p); Stv1p is located in V-ATPase complexes of the Golgi and endosomes while Vph1p is located in V-ATPase complexes of the vacuole	S223; S228	S223	CTK1		7, 32, 122, 142, 152, 217, 370, 374, 379
AKL1	Ser-Thr protein kinase; member (with Ark1p and Prk1p) of the Ark kinase family; involved in endocytosis and actin cytoskeleton organization	S407; S504; S541	S504	CLB2, CDC28		7, 32, 56, 142, 152, 374, 379

			S801	CLB2, CDC28		7, 37, 116, 142, 217, 373, 379
			S1072	AKL1		7, 32, 34, 142, 152, 217, 338, 370, 374, 379
RTG3	bHLH/Zip transcription factor for retrograde (RTG) and TOR pathways; forms a complex with another bHLH/Zip protein, Rtg1p, to activate the pathways; target of Hog1p		S371		CMP2	32, 37
ECM21	Protein involved in regulating endocytosis of plasma membrane proteins; identified as a substrate for ubiquitination by Rsp5p and deubiquitination by Ubp2p; promoter contains several Gcn4p binding elements; ECM21 has a paralog, CSR2, that arose from the whole genome duplication	S18; T20; S136; S140; S306; T959; S962; S1027; T1028; S1030	S33	CLB2, CDC28		32, 116, 142, 373, 379
			S550	DUN1		7, 52, 142
			S1030	CDC28		7, 32, 142, 152, 308, 370, 379
			T1028	CDC28		7, 142, 152, 379
HEK2	RNA binding protein involved in asymmetric localization of ASH1 mRNA; represses translation of ASH1 mRNA, an effect reversed by Yck1p-dependent phosphoryation; regulates telomere position effect and length; similarity to hnRNP-K	S252; S358; S360; S362	S252		YVH1	7, 32, 370, 374, 379
			S358	YCK1		7, 56, 142, 301, 374
			S360	YCK1		7, 142, 217, 301, 370, 374
			S362	YCK1		7, 142, 301, 370, 379
			S381	YCK1		301
			T352	YCK1		301

			T355	YCK1	301
NCL1	S-adenosyl-L-methionine-dependent tRNA: m5C-methyltransferase; methylates cytosine to m5C at several positions in tRNAs and intron-containing pre-tRNAs; increases proportion of tRNALeu(CAA) with m5C at wobble position in response to hydrogen peroxide, causing selective translation of mRNA from genes enriched in TTG codon; loss of NCL1 confers hypersensitivity to oxidative stress; similar to Nop2p and human proliferation associated nucleolar protein p120	T415; S423; S424; S431; T664; T665; S667; T671; T673; T675; S676; T677	S424	MKK2	7, 32, 116, 142, 373, 374, 379
			T426	CDC28	7, 32, 142, 379
IST2	Cortical ER protein involved in ER-plasma membrane tethering; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to the plasma membrane (PM) and regulate PM phosphatidylinositol-4-phosphate (PI4P) levels by controlling access of Sac1p phosphatase to its substrate PI4P in the PM; localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process	T701; S704; T712; S714; T726; S729; Y730; T736; S757; S763; S764; S767; S768; S844; S847; T850; T853	S764	CTK1	32, 374
			S767	YPK1	7, 32, 374, 379
SDS24	Protein involved in cell separation during budding; one of two S. cerevisiae homologs (Sds23p and Sds24p) of the S. pombe Sds23 protein, which is implicated in APC/cyclosome regulation; may play an indirect role in fluid-phase endocytosis; protein abundance increases in response to DNA replication stress; SDS24 has a paralog, SDS23, that arose from the whole genome duplication	T90; T92; S94; S98; S404; T441; S447; S458	S94	CTK1	7, 32, 56, 116, 142, 373, 379

			S458	CDC28		7, 142, 217, 370, 374, 379
TPS3	Regulatory subunit of trehalose-6-phosphate synthase/phosphatase; involved in synthesis of storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway; TPS3 has a paralog, TSL1, that arose from the whole genome duplication	S51; S52; T55; S56; S58; S59; Y61; S148; S150; S154; S181; S195	S148	CDC28		7, 32, 122, 142, 152, 217, 374, 379
TSL1	Large subunit of trehalose 6-phosphate synthase/phosphatase complex; Tps1p-Tps2p complex converts uridine-5'-diphosphoglucose and glucose 6-phosphate to trehalose; contributes to survival to acute lethal heat stress; mutant has aneuploidy tolerance; protein abundance increases in response to DNA replication stress; TSL1 has a paralog, TPS3, that arose from the whole genome duplication	S49; S53; S56; S71; S73; S77; S79; S85; S86; T87; T88; T115; S118; S135; S137; S138; S147; S155; S157; S161; S186; T191; S192; T194; S195; T205; T215; S216; T219; S220	S49	CKA1		7, 32, 122, 142, 379
			S77	CDC28	CDC28	7, 32, 100, 122, 139, 142, 370, 374, 379
			S79	MCK1		7, 32, 142, 370
			S135	CDC28		7, 32, 139, 142
			S147	CDC28	CDC28	7, 32, 139, 142, 370, 374, 379
			S155	MCK1		32, 142
			S157	MCK1		32
			S161	CDC28	CDC28	7, 32, 122, 139, 142, 374, 379

LEO1	Component of the Paf1 complex; which associates with RNA polymerase II and is involved in histone methylation; plays a role in regulating Ty1 transposition; involved in transcription elongation as demonstrated by the G-less-based run-on (GLRO) assay	S132; S358; S372; T374	S34	MEC1, TEL1		370
			S132		CMP2	7, 32, 116, 142, 217, 373, 379
			S339	MEC1, TEL1		52, 370, 379
RCK2	Protein kinase involved in response to oxidative and osmotic stress; identified as suppressor of S. pombe cell cycle checkpoint mutations; similar to CaM (calmodulin) kinases; RCK2 has a paralog, RCK1, that arose from the whole genome duplication	S186; S187	S46	CDC28		7, 32, 56, 116, 122, 142, 152, 370, 373, 374, 379
			S520	HOG1		31, 159, 391
			T379	HOG1		391
RFC1	Subunit of heteropentameric Replication factor C (RF-C); RF-C is a DNA binding protein and ATPase that acts as a clamp loader of the proliferating cell nuclear antigen (PCNA) processivity factor for DNA polymerases delta and epsilon	S40; S79; S80; T82; S88	T48	CLB2, CDC28		7, 142, 379
SIC1	Cyclin-dependent kinase inhibitor (CKI); inhibitor of Cdc28-Clb kinase complexes that controls G1/S phase transition, preventing premature S phase and ensuring genomic integrity; phosphorylated by Clb5/6-Cdk1 and Cln1/2-Cdk1 kinase which regulate timing of Sic1p degradation; phosphorylation targets Sic1p for SCF(CDC4)-dependent turnover; functional homolog of mammalian Kip1	S191	S69			33, 188, 262, 283, 287, 295, 414
			S76			33, 188, 261, 262, 283, 287, 295, 414, 441

	S80		37, 188, 262, 283, 414
	S145		37, 97, 122, 283, 295, 354, 414
	S191		7, 32, 37, 116, 122, 139, 142, 152, 272, 283, 373, 374, 414
	S201		7, 23, 37, 61, 64, 65, 116, 139, 142, 217, 374, 379
	T2	CDC28	33, 139, 283, 287, 295, 414
	T5		7, 139, 283, 287, 414
	T33		37, 97, 262, 283, 287, 354, 413, 414
	T45		37, 97, 262, 354, 379
	T48		33, 261, 262, 283, 295, 354, 414
	T173		7, 32, 90, 97, 116, 122, 152, 217, 272, 273, 283, 295, 373, 414, 461

CIC1	Essential protein that interacts with proteasome components; has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles	S365; S366	S5	MCK1		32, 100, 370
			S7	MCK1		32, 100, 370
			S10	MCK1		7, 32, 100, 116, 370, 373
			S17	MCK1	PSR1	32, 116, 370, 373, 379
			T11	MCK1	PSR1	7, 32, 100, 116, 370, 373, 379
			T15	MCK1		32, 116, 373, 379
RSC30	Component of the RSC chromatin remodeling complex; non-essential gene required for regulation of ribosomal protein genes and the cell wall/stress response; null mutants are osmosensitive; RSC30 has a paralog, RSC3, that arose from the whole genome duplication	S150; S152	S815	MEC1, TEL1		52
YHR097C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus; YHR097C has a paralog, PAL1, that arose from the whole genome duplication	S221; S222; T223; T224; T225; S233	S222		YVH1	7, 32, 100, 116, 217, 370, 373, 379
			S315	PTK1		7, 32, 56, 116, 142, 152, 373, 379
			T313		PPQ1	7, 32, 56, 116, 142, 152, 373, 379
BZZ1	SH3 domain protein implicated in regulating actin polymerization; able to recruit actin polymerization machinery through its SH3 domains; colocalizes with cortical actin	S472	S472	SNF1		7, 32, 142, 374, 379

	patches and Las17p; interacts with type I myosins					
KEL1	Protein required for proper cell fusion and cell morphology; forms a complex with Bud14p and Kel2p that regulates Bnr1p (formin) to affect actin cable assembly, cytokinesis, and polarized growth; functions in a complex with Kel2p to negatively regulate mitotic exit, interacts with Tem1p and Lte1p; localizes to regions of polarized growth; potential Cdc28p substrate	S503; S613; S691; Y700; S704; S742; S748; T755; T1001; S1003	S67	CLB2, CDC28		7, 32, 116, 122, 142, 373, 374, 379
			S503	CDC28		7, 116, 142, 373, 379
			S613	CDC28		7, 37, 116, 122, 139, 142, 217, 370, 373, 374, 379
			S689	CDC28		7, 116, 142, 370, 373, 374, 379
TDA11	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; potential Cdc28p substrate; null mutant is sensitive to expression of the top1-T722A allele	S244	S29			7, 32, 142, 152, 379
			S244		CDC28	7, 32, 122, 139, 142
			S286			7, 32, 142, 379
			T236			7, 32, 122, 139, 142, 370, 374
NVJ1	Nuclear envelope protein; anchored to the nuclear inner membrane, that interacts with the vacuolar membrane protein Vac8p to promote formation of nucleus-vacuole junctions during piecemeal microautophagy of the nucleus (PMN)	S156; S182; T187; S188; S190; S199; T251; S285; S290	S250	SNF1	CKA2	32, 139, 370, 379

			S298	CDC28		7, 116, 142, 217, 373, 379
			T251	SNF1		7, 32, 142, 370, 374, 379
FPR3	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; affects expression of multiple genes via its role in nucleosome assembly; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; PPIase domain acts as a transcriptional repressor when tethered to DNA by lexA, and repressor activity is dependent on PPIase activity; FPR3 has a paralog, FPR4, that arose from the whole genome duplication		S80	KSP1	CMP2	7, 32, 37, 116, 142, 152, 217, 373, 433
			S81	KSP1	CMP2	7, 32, 37, 116, 142, 152, 217, 373
			S186	CKA1, CKA2		426
			T89	SSK2		32, 142
			Y184	CKA1, CKA2, CKB1, CKB2	MSG5	243, 425, 426
SEC31	Component of the Sec13p-Sec31p complex of the COPII vesicle coat; COPII coat is required for vesicle formation in ER to Golgi transport; mutant has increased aneuploidy tolerance	T996; S997; S999	S836	CDC28		7, 116, 122, 142, 373, 379
			S974	RAD53		7, 100, 142, 370, 374, 379
			S980	CDC28		7, 32, 100, 142, 374, 379
			S988	KIN82		32, 142, 379

			S992	KIN82	PKC1	7, 32, 100, 139, 142, 217, 374, 379
HAL5	Putative protein kinase; overexpression increases sodium and lithium tolerance, whereas gene disruption increases cation and low pH sensitivity and impairs potassium uptake, suggesting a role in regulation of Trk1p and/or Trk2p transporters; HAL5 has a paralog, KKQ8, that arose from the whole genome duplication		S64	CDC28		142, 152
			S229	MCK1		32
			S233	MCK1		7, 32, 142, 370, 374, 379
UME6	Rpd3L histone deacetylase complex subunit; key transcriptional regulator of early meiotic genes; involved in chromatin remodeling and transcriptional repression via DNA looping; binds URS1 upstream regulatory sequence, represses transcription by recruiting conserved histone deacetylase Rpd3p (through co-repressor Sin3p) and chromatin-remodeling factor Isw2p; couples metabolic responses to nutritional cues with initiation and progression of meiosis, forms compl	S316; S318; S321; T403	S107	MCK1, MRK1, RIM11		32, 142, 379, 436
			S316	FRK1		7, 32, 142, 152, 217, 379
			T99	MCK1, MRK1, RIM11		32, 142, 244, 379, 436
			T103	MCK1, MRK1, RIM11		32, 379, 436
YCF1	Vacuolar glutathione S-conjugate transporter; ABC-C transporter of the ATP-binding cassette family; required for vacuole fusion; forms stable complexes with vacuole fusion	S251; S869; S872; S903	S251	CKA1, CKA2	CKA2	7, 56, 116, 139, 142, 302, 303,

	machinery; regulates Vam7p recruitment to vacuoles; role in detoxifying metals (Cd, Hg, As); transports GSSG that is not immediately reduced in cytosol to vacuole; transports unconjugated bilirubin, selenodigluthatione, oxidized glutathione; similar to human cystic fibrosis protein CFTR					313, 370, 373, 379
			S908	TPK1	TPK2	7, 88, 139, 142, 152, 217, 302, 370, 374, 379, 382
CAT8	Zinc cluster transcriptional activator; necessary for derepression of a variety of genes under non-fermentative growth conditions, active after diauxic shift, binds carbon source responsive elements; relative distribution to the nucleus increases upon DNA replication stress	S173	S562	SNF1		48
YMR124W; EPO1	Protein involved in septin-ER tethering; interacts with ER membrane protein, Scs2p, and Shs1p, a septin ring component, at bud neck to create ER diffusion barrier; GFP-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; interacts with Crm1p in two-hybrid assay; YMR124W has a paralog, YLR031W, that arose from the whole genome duplication	Y355; S356	S586	CLB2, CDC28		142, 379
NUP60	FG-nucleoporin component of central core of the nuclear pore complex; contributes directly to nucleocytoplasmic transport and maintenance of the nuclear pore complex (NPC) permeability barrier and is involved in gene tethering at the nuclear periphery; relocalizes to the cytosol in response to hypoxia; both NUP1 and NUP60 are homologous to human NUP153	S70; S78; S81; S312	S162	PTK1		7, 32, 116, 142, 373, 379
			S222	CLB2, CDC28		142, 379

			S312	CDC28		7, 32, 116, 142, 370, 373, 379
			S360	RAD53		7, 56, 152, 370, 379
			S382	CDC28, RAD53		7, 32, 56, 122, 142, 370, 374, 379
			S480	RAD53		7, 52, 56, 116, 370, 373, 379
			S483	RAD53		7, 52, 56, 379
			T460	CDC28		7, 32, 116, 142, 370, 373, 379
TIF4631	Translation initiation factor eIF4G; subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); interacts with Pab1p and with eIF4A (Tif1p); also has a role in biogenesis of the large ribosomal subunit; TIF4631 has a paralog, TIF4632, that arose from the whole genome duplication	S163; S191; S194; S195; S232; T241; T242; T276	S522	KSP1	SIW14	32, 152, 379
TIF4632	Translation initiation factor eIF4G; subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); TIF4632 has a paralog, TIF4631, that arose from the whole genome duplication		T196	CDC28		7, 116, 139, 142, 370, 373, 374, 379
			T301	CDC28		142, 217
RPH1	JmjC domain-containing histone demethylase; targets tri- and dimethylated H3K36; associates with actively transcribed regions and promotes elongation; repressor of autophagy-related genes in nutrient-replete conditions; damage-responsive repressor of PHR1; phosphorylated by the Rad53p-	S459; S557; S561; S688; S689	S139	RAD53		52, 142

	dependent DNA damage checkpoint pathway and by a Rim1p-mediated event during starvation; target of stress-induced hormesis; RPH1 has a paralog, GIS1, that arose from the whole genome duplication					
			S430	CDC28		7, 32, 139, 142, 152, 379
			S561	CDC28		7, 32, 116, 142, 152, 217, 373, 379
			S575	CDC28		7, 142, 379
BEM2	Rho GTPase activating protein (RhoGAP); involved in the control of cytoskeleton organization and cellular morphogenesis; required for bud emergence; potential GAP for Rho4p		T1038	CDC28		142, 379
BOI2	Protein implicated in polar growth, functionally redundant with Boi1p; interacts with bud-emergence protein Bem1p; contains an SH3 (src homology 3) domain and a PH (pleckstrin homology) domain; BOI2 has a paralog, BOI1, that arose from the whole genome duplication	T372; S373; S375; S666; S667	S450	CDC28		32, 142, 217
			S457	CDC28		32, 142, 217
			S519	CDC28	CDC28	7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 374, 379
			S523	CDC28	CDC28	7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 374, 379

			S652	CLB2, CDC28			7, 122, 139, 142, 217, 374, 379
GIP2	Putative regulatory subunit of protein phosphatase Glc7p; involved in glycogen metabolism; contains a conserved motif (GVNK motif) that is also found in Gac1p, Pig1p, and Pig2p; GIP2 has a paralog, PIG2, that arose from the whole genome duplication		S213	CDC28			142
YER079W	Putative protein of unknown function	T31; S39; S41; Y186; S189; S192; S194; S197; T201	S39			SIT4	7, 32, 139, 142
			S41	CDC28		SIT4	7, 32, 142, 374, 379
			S189	TPK3			7, 32, 142, 370, 379
			S192	TPK3			7, 32, 142, 370, 379
			S194	CKA1			7, 32, 142, 379
			T53			SIT4	32
SCS2	Integral ER membrane protein, regulates phospholipid metabolism; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to plasma membrane (PM) and regulate PI4P levels by controlling access of Sac1p phosphatase to substrate PI4P in the PM; interacts with FFAT motifs in Opi1p, Swh1p, Osh2p, and Osh3p; involved in telomeric silencing; VAP homolog; SCS2 has a paralog, SCS22, that arose from the whole genome duplication	T204	T204	CLB2, CDC28			32, 142, 379
YTA7	Protein that localizes to chromatin; has a role in regulation of histone gene expression; has a bromodomain-like region that interacts with the N-terminal tail of histone H3, and an ATPase domain; relocalizes to the cytosol in response to hypoxia; potentially phosphorylated by Cdc28p	S11; S1142	S1142	MEC1, TEL1	CKA2		7, 32, 37, 52, 116, 139, 142, 369, 370, 373, 374, 379

PFK26	6-phosphofructo-2-kinase; inhibited by phosphoenolpyruvate and sn-glycerol 3-phosphate; has negligible fructose-2,6-bisphosphatase activity; transcriptional regulation involves protein kinase A	S42; S43; S667; S671; S673; S674; S675	S652	TPK1			7, 139, 142, 217, 370, 379
			T157	TPK1			7, 56, 82, 142, 217, 370, 379
VHS2	Regulator of septin dynamics; involved in the regulation of septin dynamics at bud neck after mitotic entry, likely by stabilizing septin structure; regulated at post-translational level by cell cycle dependent phosphorylation; likely phosphorylated by Cdc28p and dephosphorylated by Cdc14p before cytokinesis; high-copy suppressor of synthetic lethality of sis2 sit4 double mutant; VHS2 has a paralog, MLF3, that arose from the whole genome duplication		S202			SIT4	32, 142
			S301	CDC28	CDC28		7, 139, 142, 152, 217, 374, 379
			S325			PTP1	32, 142, 152, 217
			S330			PTP1	32, 142, 152
AIM21	Protein of unknown function; involved in mitochondrial migration along actin filament; may interact with ribosomes; GFP-fusion protein colocalizes with Sac1p to the actin cytoskeleton	S36; T40; T84; S119; T121; T180; S183; S185; S281; T282; S476; S477; T480; T552	S183	PSK2			7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			T180	PSK2			7, 32, 142, 152, 217, 370, 374, 379
BUD6	Actin- and formin-interacting protein; participates in actin cable assembly and organization as a nucleation-promoting factor (NPF) for formins Bni1p and Bnr1p; a triple	S233	S327	CDC28			7, 12, 32, 116, 142, 217, 370,

	helical coiled-coil domain in the C-terminal region interacts with Bni1p; involved in polarized cell growth; isolated as bipolar budding mutant; potential Cdc28p substrate			373, 374, 379
MAF1	Highly conserved negative regulator of RNA polymerase III; involved in tRNA processing and stability; inhibits tRNA degradation via rapid tRNA decay (RTD) pathway; binds N-terminal domain of Rpc160p subunit of Pol III to prevent closed-complex formation; regulated by phosphorylation mediated by TORC1, protein kinase A, Sch9p, casein kinase 2; localizes to cytoplasm during vegetative growth and translocates to nucleus and nucleolus under stress conditions	S90	TPK1	7, 32, 142, 203, 267, 374, 379
		S101	TPK1	203, 267, 379
		S159	CKA1, CKA2, CKB1, CKB2	119, 379
		S160	CKA1, CKA2, CKB1, CKB2	119
		S161	CKA1, CKA2, CKB1, CKB2	119
		S162	CKA1, CKA2, CKB1, CKB2	119
		S177	TPK1	32, 56, 142, 152, 203, 267
		S178	TPK1	32, 142, 152, 203, 267, 379
		S179	SCH9	32, 152, 379

			S209	TPK1	142, 203, 217, 267, 374
			S210	TPK1	7, 203, 217, 267
			S388	CKA1, CKA2, CKB1, CKB2	119
VNX1	Calcium/H+ antiporter localized to the endoplasmic reticulum membrane; member of the calcium exchanger (CAX) family; potential Cdc28p substrate	S110; T118; S120; S121	S121	CLB2, CDC28	7, 116, 142, 152, 189, 217, 373, 379
			T118	CLB2, CDC28	142
YFL042C; LAM5	Putative sterol transfer protein; one of six StART-like domain-containing proteins in yeast that may be involved in sterol transfer between intracellular membranes; conserved across eukaryotes; has both GRAM and StART-like (VASt) domains; localizes to membrane contact sites throughout the cell, including nucleus-vacuole junctions and ER-mitochondrial contact sites	T110	S103	CDC28	142, 379
			S149	CDC28	142, 217, 379
			T110	CDC28	7, 142, 152, 217, 379
BLM10	Proteasome activator; binds the core proteasome (CP) and stimulates proteasome-mediated protein degradation by inducing gate opening; required for sequestering CP into proteasome storage granule (PSG) during quiescent phase and for nuclear import of CP in proliferating cells; required for resistance to bleomycin, may be involved in protecting against oxidative damage; similar to mammalian PA200	S11; S29; S34; S35; S36; S62; T64	S11	CDC28	7, 116, 142, 181, 373
			S29	CLB2, CDC28	7, 32, 56, 116, 142,

						181, 373, 374, 379
			S56	BUD32		7, 32, 56, 100, 139, 142, 152, 181, 217, 370, 374, 379
YPI1	Regulatory subunit of the type I protein phosphatase (PP1) Glc7p; Glc7p participates in the regulation of a variety of metabolic processes including mitosis and glycogen metabolism; in vitro evidence suggests Ypi1p is an inhibitor of Glc7p while in vivo evidence suggests it is an activator; overproduction causes decreased cellular content of glycogen; partial depletion causes lithium sensitivity, while overproduction confers lithium-tolerance	S133	S131	PSK1	CLA4	7, 32, 37, 56, 116, 139, 142, 217, 370, 373, 374
			S133	PSK1		7, 32, 37, 56, 116, 122, 142, 217, 370, 373, 374, 379
IGD1	Cytoplasmic protein that inhibits Gdb1p glycogen debranching activity; required for normal intracellular accumulation of glycogen; phosphorylated in vivo; expression increases during wine fermentation; protein abundance increases in response to DNA replication stress; IGD1 has a paralog, YOL024W, that arose from the whole genome duplication	S14	S95	TPK3		7, 32, 100, 142, 370
LSB3	Protein containing a C-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization; protein abundance increases in response to DNA replication stress; LSB3	T298; S300; S303; S311; S397; S399; T400; S401; S402	S255	CKA1		32

	has a paralog, YSC84, that arose from the whole genome duplication					
			S256	CKA1		32
SUM1	Transcriptional repressor that regulates middle-sporulation genes; required for mitotic repression of middle sporulation-specific genes; also acts as general replication initiation factor; involved in telomere maintenance, chromatin silencing; regulated by pachytene checkpoint	S378	S379	CDC28		7, 142, 152, 228, 370, 379
			S712	MEC1, TEL1		7, 52, 142, 370, 379, 527
			S738	CLB2, CDC28		7, 142, 228, 370, 374, 379
			T306	IME2		3, 271
IDS2	Protein involved in modulation of Ime2p activity during meiosis; appears to act indirectly to promote Ime2p-mediated late meiotic functions; found in growing cells and degraded during sporulation	S130; S136	S130	CDC28		7, 122, 142, 374
MTC1	Protein of unknown function that may interact with ribosomes; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to COPI-coated vesicles (early Golgi); mtc1 is synthetically lethal with cdc13-1	T330; S336; S337; S339; S340; S342	S273		YCH1	7, 32, 139, 142, 217, 379
ALY2	Alpha arrestin; controls nutrient-mediated intracellular sorting of permease Gap1p; interacts with AP-1 subunit Apl4p; phosphorylated by Npr1p and also by cyclin-CDK complex Pcl7p-Pho85p; promotes endocytosis of plasma membrane proteins; ALY2 has a paralog, ALY1, that arose from the whole genome duplication	S155; S168; S172; S213; S740; S741	S176	CLB2, CDC28		142
			S213	CDC28		7, 32, 122, 142, 152, 374, 379

BBC1	Protein possibly involved in assembly of actin patches; interacts with an actin assembly factor Las17p and with the SH3 domains of Type I myosins Myo3p and Myo5p; localized predominantly to cortical actin patches	S77; S78; T81; S83; S103; S158; S620; S621; T624; T810; S815; T818; T820; S822; T824; T835; T894; T895; S902	S103	CDC28	PHO85	7, 32, 56, 116, 139, 142, 217, 370, 373, 374, 379
			S631	MKK1		7, 32, 122, 142, 152, 217, 379
			S634	MKK1		7, 32, 142, 152, 217, 379
			S638	MKK1		32, 116, 122, 142, 152, 217, 373, 379
			T636	MKK1		32, 116, 122, 142, 152, 373, 379
PTK2	Serine/threonine protein kinase; involved in regulation of ion transport across plasma membrane; carboxyl terminus is essential for glucose-dependent Pma1p activation via phosphorylation of Pma1p-Ser899; enhances spermine uptake; PTK2 has a paralog, PTK1, that arose from the whole genome duplication	T56; S57; S59; S61; S63; S65; S69; S73; S585; T586; S587; T588; S592; S595; S711; S726; T727; T729; T730; T732; S773; S775; S776	S69	CLB2, CDC28		37, 142, 152, 379
			S711	PTK2	CKA2	7, 32, 37, 139, 142, 217, 374, 379
			S752	PTK2		7, 32, 116, 142, 217,

					373, 374, 379
			S755	PTK2	32, 142, 217, 379
			S784	CLB2, CDC28	7, 32, 37, 142, 379
			T727	CDC28	142, 217
			T730	CDC28	7, 37, 116, 142, 217, 373, 379
			T737	CDC28	116, 142, 217, 373, 379
ENT3	Protein containing an N-terminal epsin-like domain; involved in clathrin recruitment and traffic between the Golgi and endosomes; associates with the clathrin adaptor Gga2p	S148	S203	BUD32	7, 32, 142, 152, 217, 379
ASK10	Regulator of the Fps1p glycerol channel; under nonstress conditions, binds to Fps1p to positively regulate glycerol transport; under osmotic stress, multiple phosphorylation by Hog1p causes Ask10p to dissociate from Fps1p; forms homodimers and heterodimerizes with paralog Rgc1p; phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p; associates with RNA polymerase II holoenzyme	S1070	T808	CDC28	7, 32, 37, 142, 152, 379
SEC16	COPII vesicle coat protein required for ER transport vesicle budding; essential factor in endoplasmic reticulum exit site (ERES) formation, as well as in COPII-mediated ER-to-Golgi traffic; bound to periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p	S28; S30; T2127; S2128; S2130; T2132	S607	CDC28	7, 116, 122, 142, 370, 373, 379
			S841	CTK1	32, 152, 217, 379
			S1515	CDC28	7, 32, 122, 142, 152,

					217, 374, 379
CLA4	Cdc42p-activated signal transducing kinase; member of the PAK (p21-activated kinase) family, along with Ste20p and Skm1p; involved in septin ring assembly, vacuole inheritance, cytokinesis, sterol uptake regulation; phosphorylates Cdc3p and Cdc10p; CLA4 has a paralog, SKM1, that arose from the whole genome duplication	Y812; S815; T816	S445		7, 142, 152, 370, 374, 379
LYS20	Homocitrate synthase isozyme and functions in DNA repair; catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; LYS20 has a paralog, LYS21, that arose from the whole genome duplication	T396	T396	CDC28	7, 32, 56, 116, 122, 142, 152, 217, 370, 373, 374, 379
PSP2	Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of group II intron-splicing defects of a mutation in MRS2 and of a conditional mutation in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing		S340	CDC28	7, 32, 139, 142, 217, 374, 379
ACS2	Acetyl-coA synthetase isoform; along with Acs1p, acetyl-coA synthetase isoform is the nuclear source of acetyl-coA for histone acetylation; mutants affect global transcription; required for growth on glucose; expressed under anaerobic conditions		S679	MEC1, TEL1	7, 52
MDS3	Putative component of the TOR regulatory pathway; negative regulator of early meiotic gene expression; required, with Pmd1p, for growth under alkaline conditions; has an N-terminal kelch-like domain; MDS3 has a paralog, PMD1, that arose from the whole genome duplication	S668; S669; S671; S693; S781; S918; S919; T920; T923; T1156; S1166; T1168	S693	CDC28	7, 32, 37, 116, 142, 217, 370, 373, 374, 379
			S1387	CLB2, CDC28	142, 379
SDS23	Protein involved in cell separation during budding; one of two S. cerevisiae homologs	S61; T66; S398; S399; S400;	T405	CDC28	142, 217, 379

	(Sds23p and Sds24p) of the S. pombe Sds23 protein, which is implicated in APC/cyclosome regulation; SDS23 has a paralog, SDS24, that arose from the whole genome duplication	S402; S404; T405; T409; T410; S430				
YGR054W	Eukaryotic initiation factor eIF2A; associates specifically with both 40S subunits and 80 S ribosomes, and interacts genetically with both eIF5b and eIF4E; homologous to mammalian eIF2A	S473; S560; S561; T563; S564; S567; T568; S572; T581; T586; S587	S560	MCK1	TPK1	7, 32, 139, 142, 370, 374
			S561	MCK1		7, 32, 142, 370, 374
			S564	MCK1		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			T563	MCK1		7, 32, 116, 142, 152, 217, 370, 373, 374
			T568	MCK1		7, 32, 142, 379
DAM1	Essential subunit of the Dam1 complex (aka DASH complex); cooperates with Duo1p to connect the DASH complex with the microtubules (MT); couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; Ipl1p target for regulating kinetochore-MT attachments		S20	IPL1		49, 139, 142, 177, 254, 374, 379, 392
			S257	IPL1		49, 142, 177, 254, 374, 379
			S265	IPL1		49, 142, 177, 254, 379

			S292	IPL1		49, 142, 177, 374, 379
YGR130C	Component of the eisosome with unknown function; GFP-fusion protein localizes to the cytoplasm; specifically phosphorylated in vitro by mammalian diphosphoinositol pentakisphosphate (IP7)	S44; S249; T254; S257; T277; T278; S281; S284; S286; T337; S338; T339; T342	S343	TPK3		32, 217, 370, 379
			S347	YPK1		32, 217, 370, 379
HHO1	Histone H1, linker histone with roles in meiosis and sporulation; decreasing levels early in sporulation may promote meiosis, and increasing levels during sporulation facilitate compaction of spore chromatin; binds to promoters and within genes in mature spores; may be recruited by Ume6p to promoter regions, contributing to transcriptional repression outside of meiosis; suppresses DNA repair involving homologous recombination	S130; S173; S174; S176; S177	S130		SIW14	32, 116, 373
FPK1	Ser/Thr protein kinase; phosphorylates several aminophospholipid translocase family members, regulating phospholipid translocation and membrane asymmetry; phosphorylates and inhibits upstream inhibitory kinase, Ypk1p; localizes to the cytoplasm, early endosome/TGN compartments and thplasma membrane; localizes to the shmoo tip where it has a redundant role in the cellular response to mating pheromone; FPK1 has a paralog, KIN82, that arose from the whole genome duplication	S200; S462; T674; S676	S137	CDC28		7, 32, 142, 152, 379
			S140	CDC28		7, 32, 142, 152, 379
			S144	CDC28		32, 142, 152, 379

			S175	CDC28	7, 142
			S198	CDC28	7, 142
			S339	CDC28	7, 142, 152, 370, 379
			T201	CDC28	142, 217
SQS1	Protein that stimulates the ATPase and helicase activities of Prp43p; acts with Prp43p to stimulate 18s rRNA maturation by Nob1p; overexpression antagonizes the suppression of splicing defects by spp382 mutants; component of pre-ribosomal particles; relocalizes from nucleus to nucleolus upon DNA replication stress	Y103; S105; S106; T107	S343	CDC28	7, 32, 139, 142, 152, 217, 370, 379
			S345	HOG1	7, 139, 142, 152, 217, 379
MDG1	Plasma membrane protein; involved in G-protein mediated pheromone signaling pathway; overproduction suppresses bem1 mutations; MDG1 has a paralog, CRP1, that arose from the whole genome duplication	S160; T164; S178; T180; T181; T182; S227; T256; S257; S263; S272	S288	CKA1	7, 32, 116, 122, 142, 152, 373, 374, 379
			S291	PSK2	7, 32, 116, 122, 142, 373, 374, 379
			T290	PSK2	7, 32, 116, 142, 152, 373
CBK1	Serine/threonine protein kinase of the the RAM signaling network; Ndr/LATS family member; binds regulatory subunit Mob2p; involved in regulation of cellular morphogenesis, polarized growth, and septum destruction; phosphorylation by Cbk1p regulates localization and activity of Ace2p transcription factor and Ssd1p translational repressor; Cbk1p activity is regulated by both phosphorylation and specific localization;	S63; S66	S570	CBK1	155, 300

	relocalizes to cytoplasm upon DNA replication stress				
			T93	CLB2, CDC28	142
			T109	CLB2, CDC28	7, 142, 379
NSG2	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; NSG2 has a paralog, NSG1, that arose from the whole genome duplication	S49; S81; S82	S90	YPK1	7, 32, 100, 142, 152, 217, 370, 374, 379
			S92	YPK1	32, 142, 217, 370, 379
			S93	YPK1	7, 32, 100, 142, 152, 217, 370, 374, 379
CRZ1	Transcription factor, activates transcription of stress response genes; nuclear localization is positively regulated by calcineurin-mediated dephosphorylation; rapidly localizes to the nucleus under blue light stress; can be activated in stochastic pulses of nuclear localization in response to calcium		S409	TPK1	170
			S410	TPK1	142, 170, 370, 379
			S423	TPK1	56, 170
			S427	TPK1	7, 32, 56, 170, 379
			S429	TPK1	7, 32, 170, 379
GPD1	NAD-dependent glycerol-3-phosphate dehydrogenase; key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high-osmolarity glycerol response pathway; protein abundance increases in response to DNA	S23; S24; S25; S27	S24	CTK1	7, 32, 100, 116, 122, 142, 152, 168, 217, 294, 370, 373, 379

	replication stress; constitutively inactivated via phosphorylation by the protein kinases Ypk1p and Ypk2p, dephosphorylation increases catalytic activity; forms a heterodimer with Pnc1p to facilitate its peroxisomal import				
			S27	CTK1	7, 32, 100, 116, 122, 142, 152, 168, 217, 294, 370, 373, 374, 379
SLT2	Serine/threonine MAP kinase; coordinates expression of all 19S regulatory particle assembly-chaperones (RACs) to control proteasome abundance; involved in regulating maintenance of cell wall integrity, cell cycle progression, nuclear mRNA retention in heat shock, septum assembly; required for mitophagy, pexophagy; affects recruitment of mitochondria to phagophore assembly site; plays role in adaptive response of cells to cold; regulated by the PKC1-mediated signaling pathway		S423	RAD53	7, 37, 379, 398
			S428	MEC1, TEL1	7, 37, 398
REG1	Regulatory subunit of type 1 protein phosphatase Glc7p; involved in negative regulation of glucose-repressible genes; involved in regulation of the nucleocytoplasmic shuttling of Hxk2p; REG1 has a paralog, REG2, that arose from the whole genome duplication	S254; Y497; S570; S572; S576; T579; S582; S775; T776; S778; Y780; S976; S977; S1013; S1014	S421	CDC28	7, 32, 37, 142, 217, 370, 379
			S898	CDC28	7, 142, 379
			T896	CDC28	142, 379
UBP3	Ubiquitin-specific protease involved in transport and osmotic response; negatively regulates Ras/PKA signaling; interacts with	S398; S399; S400	S339		7, 32, 116, 327, 373, 379

	Bre5p to coregulate anterograde, retrograde transport between ER and Golgi; involved in transcription elongation in response to osmostress through phosphorylation at Ser695 by Hog1p; inhibitor of gene silencing; role in ribophagy; cleaves ubiquitin fusions but not polyubiquitin; protein abundance increases in response to DNA replication stress				
			S400		7, 32, 116, 142, 373, 374, 379
RSC4	Component of the RSC chromatin remodeling complex; found in close proximity to nucleosomal DNA; displaced from the surface of nucleosomal DNA after chromatin remodeling; acetylated (K25) by Gcn5p, altering replication stress tolerance; contains tandem bromodomains that recognize histone H3 acetylated on K14 (H3K14ac) by Gcn5p		S545	MEC1, TEL1	7, 52, 379
ROD1	Alpha-arrestin involved in ubiquitin-dependent endocytosis; activating dephosphorylation relays glucose signaling to transporter endocytosis; calcineurin dephosphorylation is required for Rsp5p-dependent internalization of agonist-occupied Ste2p, as part of signal desensitization; recruits Rsp5p to Ste2p via its 2 PPXY motifs; protein abundance increases in response to DNA replication stress; ROD1 has a paralog, ROG3, that arose from the whole genome duplication	S602; S720	S447	SNF1	11, 361
MUK1	Guanine nucleotide exchange factor (GEF); involved in vesicle-mediated vacuolar transport, including Golgi-endosome trafficking and sorting through the multivesicular body (MVB); specifically stimulates the intrinsic guanine nucleotide exchange activity of Rab family members (Vps21p/Ypt52p/Ypt53p); partially redundant with GEF VPS9; required for localization of	S67; T71; T498	S67	CDC28	7, 142, 374, 379

	the CORVET complex to endosomes; contains a VPS9 domain					
			S245	CLB2, CDC28		7, 32, 116, 142, 373, 374, 379
SVL3	Protein of unknown function; mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; relocalizes from bud neck to cytoplasm upon DNA replication stress; SVL3 has a paralog, PAM1, that arose from the whole genome duplication	S551	S551	CTK1		7, 32, 122, 142, 152, 217, 370, 374, 379
			T665	PKH3		32
HEH2	Inner nuclear membrane (INM) protein; contains helix-extension-helix (HEH) motif, nuclear localization signal sequence; targeting to the INM requires the Srp1p-Kap95p karyopherins and the Ran cycle; HEH2 has a paralog, SRC1, that arose from the whole genome duplication	S141; S145	S123	CLB2, CDC28		56, 139, 142, 370, 374, 379
STE20	Cdc42p-activated signal transducing kinase; involved in pheromone response, pseudohyphal/invasive growth, vacuole inheritance, down-regulation of sterol uptake; GBB motif binds Ste4p; member of the PAK (p21-activated kinase) family	T203; T207; T216; T408; T411; T413; S418; T546; S547; T552; S924	S206	CDC28		32, 217, 370, 379
			S269		PSR2	32, 116, 373
			S502	CLB2, CDC28		7, 37, 116, 142, 290, 373, 374, 379
			S517	CDC28		32, 37, 56, 142, 370, 379
			S547	CDC28, CLN2		32, 37, 56, 116, 142, 217, 290,

					370, 373, 374, 379
			S562	CDC28, CLN2	7, 32, 37, 56, 116, 139, 142, 217, 290, 370, 373, 374, 379
			T203	CLB2, CDC28	7, 32, 142, 217, 370, 379
			T217	CTK1	32, 370, 379
			T218	PKP2	32, 379
			T511	SNF1	32, 37, 142, 370
			T512	CLB2, CDC28	32, 37, 56, 142, 370, 379
			T777	STE20	7, 116, 142, 373, 430
TCB3	Cortical ER protein involved in ER-plasma membrane tethering; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to the plasma membrane (PM) and regulate PM phosphatidylinositol-4-phosphate (PI4P) levels by controlling access of Sac1p phosphatase to its substrate PI4P in the PM; localized to the bud via specific mRNA transport; non-tagged protein detected in a phosphorylated state in mitochondria; C-termini of Tcb1p, Tcb2p and Tcb3p interact	S1335; S1340; S1342; S1346; T1347; T1350; S1354; Y1357; S1360; T1364; Y1366; S1371; S1373; T1379; T1382; S1383; S1386	S1373	CLB2, CDC28	142, 374, 379
			T1350	CDC28	7, 32, 100, 122, 142, 152, 217, 331, 370, 374, 379
ESC1	Protein involved in telomeric silencing; required for quiescent cell telomere hypercluster localization at nuclear membrane	S532	S1145		7, 52, 122, 139, 142, 374, 379

	vicinity; interacts with PAD4-domain of Sir4p				
			S1166	PKC1	7, 52, 116, 139, 142, 152, 373
			S1348		32, 370, 379
			S1354		7, 32, 116, 142, 370, 373, 379
			T1353		32, 142, 370, 379
TAF12	Subunit (61/68 kDa) of TFIID and SAGA complexes; involved in RNA polymerase II transcription initiation and in chromatin modification, similar to histone H2A; overexpression of the human ortholog, TAF12, an oncogene involved in the formation of choroid plexus carcinomas, results in dosage chromosomal instability (dCIN) in a human cell line similar to the dCIN observed in yeast overexpressors		S325	MEC1, TEL1	7, 52, 379
NUP53	FG-nucleoporin component of central core of nuclear pore complex (NPC); also part of the NPC nuclear basket; contributes directly to nucleocytoplasmic transport; involved in regulation of transcription and mitosis; induces membrane tubulation, which may contribute to nuclear pore assembly; NUP53 has a paralog, ASM4, that arose from the whole genome duplication		S101	CDC28	7, 142, 217, 240, 370, 379
			S206	CDC28	240, 379
CUE4	Protein of unknown function; has a CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; CUE4 has a paralog, CUE1, that arose from the whole genome duplication	T32; S41; S48; S54	S48	KNS1	7, 32, 142, 370, 379
SEG1	Component of eisosome required for proper eisosome assembly; precedes Pil1p/Lsp1p during eisosome formation, controls eisosome length and shape; diffusely distributed, forms	S302; S318; S450; T452	S658	CLB2, CDC28	7, 142, 379

	heterogeneous patches at plasma membrane in small buds, also found in medium and large buds; expression repressed by cAMP; similar to A. gossypii SEG gene and to S. pombe Sle1p, important for generating eisosomes; SEG1 has a paralog, SEG2, that arose from the whole genome duplication				
			S870	CDC28	142
			T675	CLB2, CDC28	7, 32, 56, 142, 370, 374, 379
YMR196W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YMR196W is not an essential gene	T1008; S1010; T1013; S1016; S1020	S1081	CDC28	7, 139, 142, 379
MYO5	One of two type I myosin motors; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; MYO5 has a paralog, MYO3, that arose from the whole genome duplication	S357; Y359; T1034; T1036; S1038; S1040; S1045; T1048; T1051	S357	YPK2	7, 32, 56, 116, 121, 122, 142, 152, 217, 370, 373, 374, 379
GAL83	One of three possible beta-subunits of the Snf1 kinase complex; allows nuclear localization of the Snf1 kinase complex in the presence of a nonfermentable carbon source; necessary and sufficient for phosphorylation of the Mig2p transcription factor in response to alkaline stress; functionally redundant with SIP1 and SIP2 for the phosphorylation of Mig1p in response to glucose deprivation; contains a glycogen-binding domain		S64	SNF1	246
			S65	SNF1	246
			S87	CKA1, CKA2, CK1B1, CKB2	246
			S93	CKA1, CKA2,	246

				CK1B1, CKB2			
			T90	CKA1, CKA2, CK1B1, CKB2			246
GFD1	Coiled-coiled protein of unknown function; identified as a high-copy suppressor of a dbp5 mutation; protein abundance increases in response to DNA replication stress	S106	S106				7, 32, 116, 142, 217, 373, 374, 379
			S111				7, 32, 116, 142, 217, 373, 374, 379
TRI1	Non-essential sumoylated protein of unknown function; similar to components of human SWI/SNF complex including SMRD3; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, nucleus and nucleolus; TRI1 has a paralog, UAF30, that arose from the whole genome duplication	S113	S113	CDC28	CDC28		7, 139, 142, 379
EIS1	Component of the eisosome required for proper eisosome assembly; similar to Uso1p; authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies; protein increases in abundance and relocalizes from plasma membrane to cytoplasm upon DNA replication stress; EIS1 has a paralog, YKL050C, that arose from the whole genome duplication	T18; S19; S23; S26; S130; S133; S151; S179; S584; S701; Y704; T706; S710; T759; T761; S762; S763; T767; S775; S780; S781; S791; S795; S825; S828; S829; S838	S23			SIW14	32, 56, 116, 142, 370, 373, 379
			S30			SIW14	32
			S130	MCK1	SCH9		7, 32, 56, 116, 139, 142, 152, 331, 373, 374, 379

			S133	MCK1			7, 32, 56, 116, 152, 373, 379
			S136	SNF1			32, 116, 152, 373, 379
			S139	SNF1			32, 379
			S584	YPK1	TPK1		7, 32, 56, 116, 122, 139, 142, 217, 370, 373, 374, 379
			S762	PSK2		YVH1	32, 370, 374
			S763	PKP1		YVH1	7, 32, 116, 142, 152, 370, 373, 374, 379
			S775	CKA1	HRR25		7, 32, 116, 139, 142, 152, 370, 373, 379
			S791	FRK1			32
			T767	PSK2			32, 152, 379
ASM4	FG-nucleoporin component of central core of nuclear pore complex (NPC); contributes directly to nucleocytoplasmic transport; induces membrane tubulation, which may contribute to nuclear pore assembly; ASM4 has a paralog, NUP53, that arose from the whole genome duplication		S464	CDC28			142, 379
MSC3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; msc3 mutants are defective in directing meiotic recombination events to homologous chromatids; potential Cdc28p substrate; protein abundance increases in response to DNA replication stress	S80; S82; S83; T144; S151; S155; Y357; S363; T646; S648; S658; S659; S660	S46	CDC28			142

YLR257W	Protein of unknown function; protein abundance increases in response to DNA replication stress	S66; S129; S135; S137; S139; T142; S143	S197	HOG1	PKC1	PPH21	7, 32, 116, 139, 142, 217, 370, 373, 379
			S200		CKA2	PPH21	7, 32, 56, 116, 139, 370, 373, 379
			S252	PTK1			7, 32, 370, 379
			T8	FRK1			7, 32, 142, 152, 217, 374, 379
ESF1	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels	S86; S372	S86	FUS3			7, 32, 116, 139, 142, 152, 217, 373, 374, 379
			S223			CMP2	7, 32, 116, 139, 142, 217, 373, 374, 379
			T220			CMP2	32, 56, 116, 139, 373, 379
CRN1	Coronin; cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; plays a role in regulation of actin patch assembly	S456; S460; S462; S463; S465; S484; S485; T520; T565; S567; S573; T575; S578; S579; T600; S601	S463			PPH21	7, 32, 56, 116, 142, 217, 370, 373, 374, 379
RSC2	Component of the RSC chromatin remodeling complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; RSC2 has a paralog, RSC1, that arose from the whole genome duplication	S682	S682	CLB2, CDC28	CDC28		7, 32, 116, 122, 139, 142, 152, 217, 373, 374, 379

			T11	MEC1, TEL1	7, 52
			T243	CDC28	7, 32, 142, 374, 379
SPN1	Protein involved in RNA polymerase II transcription; is constitutively recruited to the CYC1 promoter and is required for recruitment of chromatin remodeling factors for the expression of CYC1 gene; interacts genetically or physically with RNAP II, TBP, TFIIS, and chromatin remodelling factors; central domain highly conserved throughout eukaryotes; mutations confer an Spt- phenotype	T15; S85; T86; S89; T120	S23	MEC1, TEL1	7, 32, 52, 116, 142, 152, 217, 370, 373, 374, 379
			S89	SSK2	7, 32, 56, 116, 142, 192, 217, 370, 373, 374, 379
			S118	KNS1	32, 370, 379
VIP1	Inositol hexakisphosphate and inositol heptakisphosphate kinase; inositol heptakisphosphate (IP7) production is important for phosphate signaling; involved in cortical actin cytoskeleton function, and invasive pseudohyphal growth analogous to S. pombe asp1; inositol hexakisphosphate is also known as IP6	T143; S145	S141	MKK2	7, 32, 116, 142, 217, 370, 373, 374, 379
			S1107	CDC28	7, 32, 37, 116, 122, 142, 373, 374, 379
			S1121	PTK1	32
NVJ2	Lipid-binding ER protein, enriched at nucleus-vacuolar junctions (NVJ); may be involved in sterol metabolism or signaling at the NVJ; contains a synaptotagmin-like-mitochondrial-lipid binding protein (SMP) domain; binds phosphatidylinositols and other lipids in a large-scale study; may interact with	S591; S621; S622; T624; S640; S646	S676	CDC28	7, 122, 142, 217, 370, 379

	ribosomes, based on co-purification experiments					
HBT1	Shmoo tip protein, substrate of Hub1p ubiquitin-like protein; mutants are defective for mating projection formation, thereby implicating Hbt1p in polarized cell morphogenesis; HBT1 has a paralog, YNL195C, that arose from the whole genome duplication	Y29; S41; S43; T45; S251; T259; S301; S303; Y362; S363; S427; Y428; S431; S795; S843; S850; Y855; S856; S857; S932; T939; T940; S941; Y942; S943; T948; T949; S950; S956; S959; S962; S983; S990; T991; S993; Y1003; S1005; S1036	S41	SAT4		7, 32, 116, 142, 373
			S43	PBS2		32, 116, 142, 373
			S251		SIW14	32
			S257		SIW14	32
			S301	PSK2		32, 142
			S303	MCK1		32, 142, 370, 374
			S363	PKP1	PPH22	7, 32, 56, 116, 142, 370, 373
			S561		PPH22	32, 142
			S671	CDC28	PPS1	32, 142
			S856	PKP1		32, 142
			S857	MCK1	PPH22	32, 142, 374
			S956	MCK1		7, 32, 100, 116, 142, 370, 373, 374

			S959	MCK1		PPH22	32, 100, 116, 142, 373, 374
			S962	PKP1		PPH22	32, 100, 116, 142, 373, 374
			S990	CMK1			32
			S1034	PKP1	CLA4		7, 32, 116, 122, 139, 142, 217, 373
			S1036	CLA4		PPH22	7, 32, 116, 122, 142, 373
			T366	PSK2			7, 32, 370
			T368	PKP1			32
			T949	PBS2			32
			T991	PKP1			32
			T997	MCK1			32, 56, 100, 142
			Y362	PBS2			32
			Y987	MCK1			32
VPS13	Protein involved in prospore membrane morphogenesis; peripheral membrane protein that localizes to the prospore membrane and at numerous membrane contact sites; involved in sporulation, vacuolar protein sorting, prospore membrane formation during sporulation, and protein-Golgi retention; required for mitochondrial integrity; contains a PH-like domain; homologous to human CHAC and COH1 which are involved in Chorea-acanthocytosis and Cohen syndrome, respectively	T433; S436; T438; T440	S1715	RCK2	PKC1		7, 32, 122, 139, 142, 217, 370, 379
			T1379	CDC28	CDC28		7, 32, 100, 139, 142, 379
ZEO1	Peripheral membrane protein of the plasma membrane; interacts with Mid2p; regulates the cell integrity pathway mediated by Pkc1p	S40; T49	S85	BUD32			32, 116, 152, 373

	and Slt2p; the authentic protein is detected in a phosphorylated state in highly purified mitochondria				
			S89	PTK1	32, 116, 152, 373, 379
			T49	VPS34	7, 32, 56, 116, 122, 139, 142, 217, 331, 370, 373, 379
CUE5	Ubiquitin-binding protein; functions as ubiquitin-Atg8p adaptor in ubiquitin-dependent autophagy; serves as proteaphagy receptor for inactivated 26S proteasomes; contains CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; CUE5 has a paralog, DON1, that arose from the whole genome duplication; human TOLLIP is a functional CUE-domain homolog, can complement yeast null mutant, rescuing hypersensitivity of cue5 null mutant cells to Htt-96Q	S21; S36; S45; T50; T70; S220; T346; S348; S351; T352	S21	MKK1	7, 32, 116, 142, 217, 370, 373, 379
			S220	KSP1	7, 32, 142, 217, 374, 379
			T364	CLB2, CDC28	7, 32, 100, 116, 142, 152, 217, 370, 373, 379
			T367	CDC28	32, 100, 142, 152, 370, 379
			T369	CDC28	7, 32, 152
VHS3	Negative regulatory subunit of protein phosphatase 1 Ppz1p; involved in coenzyme A biosynthesis; subunit of the phosphopantothenoylcysteine decarboxylase	T108; T183; S221; S223; T224; S225	S223	RTK1	7, 32, 142, 217

	(PPCDC; Cab3p, Sis2p, Vhs3p) complex and the CoA-Synthesizing Protein Complex (CoA-SPC: Cab2p, Cab3p, Cab4p, Cab5p, Sis2p and Vhs3p)				
			S225	CDC28	7, 32, 142, 374
ALE1	Broad-specificity lysophospholipid acyltransferase; part of MBOAT family of membrane-bound O-acyltransferases; key component of Lands cycle; may have role in fatty acid exchange at sn-2 position of mature glycerophospholipids	S513	S513	PHO85	7, 32, 56, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
HRK1	Protein kinase; implicated in activation of the plasma membrane H(+)-ATPase Pma1p in response to glucose metabolism; plays a role in ion homeostasis; protein abundance increases in response to DNA replication stress		S47	HRK1	7, 32, 116, 152, 370, 373
TCO89	Subunit of TORC1 (Tor1p or Tor2p-Kog1p-Lst8p-Tco89p); regulates global H3K56ac; TORC1 complex regulates growth in response to nutrient availability; cooperates with Ssd1p in the maintenance of cellular integrity; deletion strains are hypersensitive to rapamycin	S119; S546	S497	PTK2	32, 142, 379
			S500	PTK2	32, 142, 379
			S546	CLB2, CDC28	116, 142, 217, 373, 379
SLF1	RNA binding protein that associates with polysomes; may be involved in regulating mRNA translation; involved in the copper-dependent mineralization of copper sulfide complexes on cell surface in cells cultured in copper salts; SLF1 has a paralog, SRO9, that arose from the whole genome duplication; protein abundance increases in response to DNA replication stress	S40; S41; S42	S42	CDC28	7, 32, 122, 142, 374, 379
RCN2	Protein of unknown function; green fluorescent protein (GFP)-fusion protein	S102; S104; T105; S110;	S143	SLT2	32

	localizes to the cytoplasm; phosphorylated in response to alpha factor; protein abundance increases in response to DNA replication stress	S129; T132; S149; S150; S152; S156; S157; S160; S183; S185; S186; S187; S188; T189; T200; S201; S204; T248; S250; S255; S257; T259				
			S150	SLT2	RIM11	7, 32, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S152	TPK2		7, 32, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S157	TPK2		7, 32, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S160	SLT2		7, 32, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			T132	TPK2		7, 32, 142, 217, 370
IOC2	Subunit of the Isw1b complex; exhibits nucleosome-stimulated ATPase activity and acts within coding regions to coordinate		S262	MEC1, TEL1		7, 52, 142, 379

	transcription elongation with termination and processing; contains a PHD finger motif; other complex members are Isw1p and Ioc4p						
			S605	MEC1, TEL1			52
			S760	MEC1, TEL1			52
CHS5	Component of the exomer complex; the exomer which also contains Csh6p, Bch1p, Bch2p, and Bud7, is involved in the export of select proteins, such as chitin synthase Chs3p, from the Golgi to the plasma membrane; interacts selectively with the activated, GTP-bound form of Arf1p; Chs5p is the only protein with a BRCT domain that is not localized to the nucleus	S312; S318; S321; S338; S347; T348; S365; T373; S384; S399; S400; S579; S590; S600	S347			SIT4	32, 370
			T334			SIT4	32, 142, 370, 379
MRH1	Protein that localizes primarily to the plasma membrane; also found at the nuclear envelope; long-lived protein that is asymmetrically retained in the plasma membrane of mother cells; the authentic, non-tagged protein is detected in mitochondria in a phosphorylated state; null mutation confers sensitivity to acetic acid	S289; T295; S299	S289	YPK1	CDC28	SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
			T295	PSK2	CDC28	SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
LYS21	Homocitrate synthase isozyme; catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; LYS21 has a paralog, LYS20, that arose from the whole genome duplication	S409; T410	T410	CDC28			7, 32, 56, 116, 142, 217, 370, 373, 374

DCS2	m(7)GpppX pyrophosphatase regulator; non-essential, stress induced regulatory protein; modulates m7G-oligoribonucleotide metabolism; inhibits Dcs1p; regulated by Msn2p, Msn4p, and the Ras-cAMP-cAPK signaling pathway; mutant has increased aneuploidy tolerance; DCS2 has a paralog, DCS1, that arose from the whole genome duplication	S58; S60; S63; T64; T340; S341	S63	PKH2			7, 32, 142, 370, 374
			T64	MCK1			7, 32, 116, 142, 370, 373, 374
BUG1	Cis-golgi localized protein involved in ER to Golgi transport; forms a complex with the mammalian GRASP65 homolog, Grh1p; mutants are compromised for the fusion of ER-derived vesicles with Golgi membranes	S2; S87; T275; T277	S87	CKA2			7, 32, 116, 142, 217, 370, 373, 374, 379
			T277	CDC28			142, 379
HSP42	Small heat shock protein (sHSP) with chaperone activity; forms barrel-shaped oligomers that suppress unfolded protein aggregation; involved in cytoskeleton reorganization after heat shock; protein abundance increases and forms cytoplasmic foci in response to DNA replication stress	S182; S213; S214; S215; S223; S232; T236	S213	PBS2	TPK1		7, 32, 139, 142, 152, 217, 370, 379
			S214	PBS2	SNF1	PPH21	7, 32, 116, 122, 139, 142, 152, 217, 370, 373, 379
			S215			PPH21	7, 32, 116, 122, 142, 152, 217, 370, 373, 379
			S223			PPH21	7, 32, 142, 379
STB3	Ribosomal RNA processing element (RRPE)-binding protein; involved in the glucose-induced transition from quiescence to growth;	S9; S307	S337			PTC7	32, 142, 152, 374, 379

	restricted to nucleus in quiescent cells, released into cytoplasm after glucose repletion; binds Sin3p; relative distribution to the nucleus increases upon DNA replication stress						
			S341			PTC7	32, 56, 152, 379
PAR32	Protein of unknown function; hyperphosphorylated upon rapamycin treatment in a Tap42p-dependent manner; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; PAR32 is not an essential gene		S36	PHO85			7, 32, 116, 139, 142, 152, 217, 373, 374, 379
			S39	PHO85			7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S49	PHO85			32, 152
			S131	VPS15			32
			S138			YCH1	32, 142, 152, 217, 374, 379
			S141			YCH1	32, 37, 142, 152, 217, 370, 379
			S148	CLB2, CDC28			7, 32, 142, 152
			S246	CLB2, CDC28	CDC28		7, 32, 116, 122, 139, 142, 152, 217, 373, 374, 379
ENT1	Epsin-like protein involved in endocytosis and actin patch assembly; functionally redundant with Ent2p; binds clathrin via a clathrin-binding domain motif at C-terminus; relocalizes from bud neck to cytoplasm upon DNA replication stress; ENT1 has a paralog,	T160; S163	T346	PRK1			7, 56, 116, 146, 370, 373, 374, 379

	ENT2, that arose from the whole genome duplication					
			T366	PRK1		7, 32, 142, 146, 152, 217, 370, 379
			T395	PRK1		7, 32, 122, 142, 146, 152, 217, 370, 379, 421
			T415	PRK1		146, 421
			T427	PRK1		142, 146
HRP1	Subunit of cleavage factor I; cleavage factor I is a five-subunit complex required for the cleavage and polyadenylation of pre-mRNA 3' ends; RRM-containing heteronuclear RNA binding protein and hnRNPA/B family member that binds to poly (A) signal sequences; required for genome stability	S2; S87	S462	CDC28		7, 32, 116, 122, 142, 373, 379
IGO2	Protein required for initiation of G0 program; prevents degradation of nutrient-regulated mRNAs via the 5'-3' mRNA decay pathway; phosphorylated by Rim15p; GFP protein localizes to the cytoplasm and nucleus; IGO2 has a paralog, IGO1, that arose from the whole genome duplication		S119		PPH22	32, 139, 142, 379
			S122		PPH22	32, 379
			S128	CLB2, CDC28		32, 142, 152, 370, 379

Table 3.3 Phosphorylated proteins and their known kinases in high and low density cells treated with LCA on day 0.

Gene Symbol	Description	PhosphoSite in Sample	PhosphoSite in Literature	Known Kinase	Predicted Kinase	Known Phosphatases	Reference
CDC19	Pyruvate kinase; functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; regulated via allosteric activation by fructose bisphosphate; CDC19 has a paralog, PYK2, that arose from the whole genome duplication	T372; T376; S377; T378	S22	TPK1			7, 104, 122, 142, 217, 317, 370, 374, 379
			T407	CDC28			7, 142, 379
GPM1	Tetrameric phosphoglycerate mutase; mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis	S116	S116	CTK1			7, 32, 56, 122, 139, 142, 217, 370, 374, 379
RAS2	GTP-binding protein; regulates nitrogen starvation response, sporulation, and filamentous growth; farnesylation and palmitoylation required for activity and localization to plasma membrane; homolog of mammalian Ras proto-oncogenes; RAS2 has a paralog, RAS1, that arose from the whole genome duplication	S225; T226; T227	T240	SNF1			7, 32, 217, 379
HTB1	Histone H2B; core histone protein required for chromatin assembly and chromosome function; nearly identical to HTB2; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates reassembly after DNA replication, transcriptional activation, meiotic DSB formation and H3 methylation		S11	STE20			4, 2005
DPS1	Aspartyl-tRNA synthetase, primarily cytoplasmic; homodimeric enzyme that catalyzes the specific aspartylation of tRNA(Asp); class II aminoacyl tRNA synthetase; binding to its own mRNA may confer autoregulation; shares five highly	S2; S14; S301	S14			SIT4	7, 32, 370, 379

	conserved amino acids with human that when mutated cause leukoencephalopathy characterized by hypomyelination with brain stem and spinal cord involvement and leg spasticity (HBSL)						
HXK2	Hexokinase isoenzyme 2; phosphorylates glucose in cytosol; predominant hexokinase during growth on glucose; represses expression of HXK1, GLK1, induces expression of its own gene; antiapoptotic; phosphorylation/dephosphorylation at Ser14 by kinase Snf1p, phosphatase Glc7p-Reg1p regulates nucleocytoplasmic shuttling of Hxk2p; functions downstream of Sit4p in control of cell cycle, mitochondrial function, oxidative stress resistance, chronological lifespan; has paralog HXK1	S15; S158	S15	TPK1	TPK1	GLC7, REG1	7, 10, 11, 29, 32, 100, 122, 138, 139, 142, 152, 179, 190, 324, 374
HTA1	Histone H2A; core histone protein required for chromatin assembly and chromosome function; one of two nearly identical subtypes (see also HTA2); DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p; N-terminally propionylated in vivo	S129	S129	MEC1			52, 85, 100, 116, 134, 183, 379, 404, 409, 435
NOT3	Component of the CCR4-NOT core complex, involved in mRNA decapping; involved in transcription initiation and elongation and in mRNA degradation; conserved lysine in human homolog of Not3p and Not5p is mutated in cancers	S304; S316; T319; S324; S325; S326; S344; S347; S348; S441; S442; S446; S450; T454; S798	S450	PHO85	RIM11		7, 32, 100, 116, 139, 142, 152, 217, 373, 374, 379
			T454	PHO85			7, 32, 100, 116, 142, 152, 217, 373, 374, 379
DED1	ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase; required for translation initiation of all yeast mRNAs; binds to mRNA cap-associated factors, and binding stimulates Ded1p RNA-dependent ATPase		S535	MCK1		SIT4	7, 32, 56, 139, 142, 152, 217, 374, 379

	activity; mutation in human homolog DBY is associated with male infertility; human homolog DDX3X complements ded1 null mutation; DED1 has a paralog, DBP1, that arose from the whole genome duplication					
			S539	MCK1	SIT4	7, 32, 56, 142, 152, 217, 374, 379
			S541	MCK1		7, 32, 142, 152, 370, 379
			S543	MCK1		7, 32, 56, 142, 152, 379
			S576	MCK1		32, 56, 142, 152, 217, 379
SNF1	AMP-activated S/T protein kinase; forms a complex with Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis; regulates nucleocytoplasmic shuttling of Hxk2p; regulates filamentous growth and acts as a non-canonical GEF, activating Arf3p during invasive growth; SUMOylation by Mms21p inhibits its function and targets Snf1p for destruction via the Slx5-Slx8 Ub ligase	T210; T408; S413	T210	ELM1	GLC7, REG1	7, 37, 92, 142, 143, 237, 250, 251, 260, 264, 284, 379, 383
TOP2	Topoisomerase II; relieves torsional strain in DNA by cleaving and re-sealing phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis; required for replication slow zone (RSZ) breakage following Mec1p inactivation; human homolog TOP2A implicated in cancers, and can complement yeast null mutant	S2; T3; T1306; T1309; T1314	S1310	KNS1		32, 116, 139, 142, 152, 217, 370, 373, 374, 379

			S1356	CKA1, CKA2			44, 108, 142, 214
			S1363	CKA1, CKA2			214
			T1250	CDC28			142, 370, 379
			T1314	KNS1	CDC28		32, 116, 139, 142, 152, 217, 370, 373, 374, 379
			T1365	CKA1, CKA2			214
BCY1	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA); PKA is a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation	S68; S70; S74; S77; S79; T129; S130; T131; T144; S145; S147; T150	S70	MCK1			7, 32, 142, 374, 379
			S89	CDC28			142
			S130	KNS1			7, 32, 142, 217, 370, 374
			S147	KIN4			32, 142, 374
			T129	KNS1			7, 32, 142, 217, 370, 374, 379
			T131	KNS1			7, 32, 142, 217, 370, 374, 379
			T144			CNA1	7, 32, 37, 40, 56, 142, 217, 374
CHO1	Phosphatidylserine synthase; functions in phospholipid biosynthesis; catalyzes the reaction CDP-diaclyglycerol + L-serine = CMP + L-1-phosphatidylserine, transcriptionally repressed by myo-inositol and choline	S34; T40; S46; S47; S50; T53; T54	S46	TPK1			7, 32, 59, 139, 142, 152, 217, 370, 374, 379

			S47	TPK1		7, 59, 122, 142, 152, 217, 370, 374, 379
FBP1	Fructose-1,6-bisphosphatase; key regulatory enzyme in the gluconeogenesis pathway, required for glucose metabolism; undergoes either proteasome-mediated or autophagy-mediated degradation depending on growth conditions; glucose starvation results in redistribution to the periplasm; interacts with Vid30p	S12; T13; T18	S12	TPK1		126, 142, 247, 332, 333
RPS23A	Ribosomal protein 28 (rp28) of the small (40S) ribosomal subunit; required for translational accuracy; homologous to mammalian ribosomal protein S23 and bacterial S12; RPS23A has a paralog, RPS23B, that arose from the whole genome duplication; deletion of both RPS23A and RPS23B is lethal	S128	S41	SNF1		32, 116, 373, 379
RPS6A; RPS6B	Protein component of the small (40S) ribosomal subunit; homologous to mammalian ribosomal protein S6, no bacterial homolog; phosphorylated on S233 by Ypk3p in a TORC1-dependent manner, and on S232 in a TORC1/2-dependent manner by Ypk1/2/3p; RPS6B has a paralog, RPS6A, that arose from the whole genome duplication		S232	YPK3		7, 32, 100, 116, 122, 142, 152, 162, 373, 379
SEC7	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors; involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles	S2; T334; S434; S437; S439; S809; T1722; S1723; S1726; S1804	S780	VPS34		7, 32, 142, 217, 374, 379
			S782	VPS34		32, 142, 379
			T1240	CDC28	CDC28	139, 142, 217, 374, 379

SCH9	AGC family protein kinase; functional ortholog of mammalian S6 kinase; phosphorylated by Tor1p and required for TORC1-mediated regulation of ribosome biogenesis, translation initiation, and entry into G0 phase; involved in transactivation of osmostress-responsive genes; regulates G1 progression, cAPK activity and nitrogen activation of the FGM pathway; integrates nutrient signals and stress signals from sphingolipids to regulate lifespan	S288; S289; S290	S711	TOR1	335, 379, 406
			S726	TOR1	7, 32, 37, 116, 142, 152, 217, 335, 373, 374, 379, 406
			S758	TOR1	176, 335, 406
			S765	TOR1	176, 335, 406
			T570	PKH1	7, 37, 46, 150, 176, 275, 315, 335, 370, 379, 406, 415
			T723	TOR1	32, 142, 152, 176, 217, 335, 379, 406
			T737	TOR1	46, 176, 275, 335, 379, 406
YPK1	S/T protein kinase; phosphorylates, downregulates flippase activator Fpk1p; inactivates Orm1p and Orm2p by phosphorylation in response to compromised sphingolipid synthesis; involved in the TORC-dependent phosphorylation of	T48; S50; S51	S51	CTK1	32, 56, 215, 217, 336, 370

	ribosomal proteins Rps6a/b (S6); mutations affect receptor-mediated endocytosis and sphingolipid-mediated and cell integrity signaling pathways; human homolog SGK1 can complement a null mutant; human homolog SGK2 can complement a ypk1 ypk2 double mutant					
			T504	PKH1		37, 46, 69, 122, 142, 215, 226, 232, 335
CAF20	Phosphoprotein of the mRNA cap-binding complex; involved in translational control; repressor of cap-dependent translation initiation; competes with eIF4G for binding to eIF4E	S91; T99; T101; T102; T104; S105; T106; T111	S58	PSK2		342
			S59	PSK2		342
			S78	FRK1		32, 116, 142, 152, 373, 379
			S91	SLT2	CKA2	7, 32, 116, 139, 142, 217, 370, 373, 374, 379, 452
			T102	SLT2		7, 32, 116, 122, 142, 217, 370, 373, 374, 379
KIN1	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; KIN1 has a paralog, KIN2, that arose from the whole genome duplication	S660; S663; S764; S937; S938	S660	SNF1		7, 32, 142, 379
			S663	SNF1		7, 32, 142, 370, 379
KIN2	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane;		S24	CDC28, CLB2		7, 37, 142, 379

	KIN2 has a paralog, KIN1, that arose from the whole genome duplication					
			S609	CDC28		7, 37, 142, 217, 379
			S643	CDC28		7, 32, 37, 116, 142, 370, 373, 374, 379
PCT1	Cholinephosphate cytidylyltransferase; a rate-determining enzyme of the CDP-choline pathway for phosphatidylcholine synthesis, inhibited by Sec14p, activated upon lipid-binding; contains an element within the regulatory domain involved in both silencing and activation of enzymatic activity	S346; T349	S346	MKK1		7, 32, 122, 139, 142, 217, 374, 379
ABF1	DNA binding protein with possible chromatin-reorganizing activity; involved in transcriptional activation, gene silencing, and DNA replication and repair	S467; S720	S193	MEC1, TEL1		7, 32, 142, 370, 379
			S720	CKA1, CKA2, CKB1, CKB2	CKA2	7, 56, 116, 139, 142, 217, 373, 374, 379, 405
CHS2	Chitin synthase II; catalyzes transfer of N-acetylglucosamine (GlcNAc) to chitin upon activation of zymogenic form; required for chitin synthesis in the primary septum during cytokinesis; localization regulated by Cdk1p during mitosis; phosphorylation by Dbf2p kinase regulates its dynamics and chitin synthesis during cytokinesis		S60	CDC28, CLB2		142, 152, 379
			S86	CDC28, CLB2		7, 32, 100, 142, 152, 370, 379
			S100	CDC28, CLB2		32, 142, 374, 379
			S133	CDC28		7, 142, 370, 379

YAK1	Serine-threonine protein kinase; component of a glucose-sensing system that inhibits growth in response to glucose availability; upon nutrient deprivation Yak1p phosphorylates Pop2p to regulate mRNA deadenylation, the co-repressor Crf1p to inhibit transcription of ribosomal genes, and the stress-responsive transcription factors Hsf1p and Msn2p; nuclear localization negatively regulated by the Ras/PKA signaling pathway in the presence of glucose	S38; T288; Y530	Y530	YAK1	7, 13, 122, 142, 152, 175, 217, 374, 379
CYC8	General transcriptional co-repressor; acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters; can form the prion [OCT+]	S421; T426; S429; S741; S768; S815; S817; S943	S780	MEC1, TEL1	7, 370
			S815	KNS1	7, 32, 142, 217, 370, 374, 379
			S819	KNS1	32, 142, 379
ABP1	Actin-binding protein of the cortical actin cytoskeleton; important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; inhibits barbed-end actin filament elongation; phosphorylation within its Proline-Rich Regio, mediated by Cdc28p and Pho85p, protects Abp1p from proteolysis mediated by its own PEST sequences; mammalian homolog of HIP-55 (hematopoietic progenitor kinase 1 [HPK1]-interacting protein of 55 kDa)	T157; S163; T165; S167; S169; S174; T181; S183; S313; S475; S478; S481	S26	PTK2	32
			S169	CDC28, CLB2	7, 32, 56, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S183	CDC28	7, 32, 56, 100, 116,

						142, 152, 217, 370, 373, 374, 379
			S313	CDC28		7, 32, 116, 142, 373, 379
			T30	PTK2		32
			T31	PTK2		32
			T165	CDC28, CLB2	PHO85	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			T181	CDC28, CLB2	PHO85	7, 32, 56, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
HSP26	Small heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation; long-lived protein that is preferentially retained in mother cells and forms cytoplasmic foci; oligomer activation requires heat-induced conformational change; also has mRNA binding activity	S2; S5; T42; S47; T48; S208; S211	S208	MEC1, TEL1		7, 52, 100, 142, 152, 379
			S211	MEC1, TEL1		7, 52, 100, 122, 139, 142, 152, 374, 379
VMA2	Subunit B of V1 peripheral membrane domain of vacuolar H+-ATPase; electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the cytoplasm; protein abundance increases in	T501; S503; S504; S511; S515	S503	SNF1		7, 32, 56, 370, 374

	response to DNA replication stress; human homolog ATP6V1B1, implicated in autosomal-recessive distal renal tubular acidosis (RTA) with sensorineural deafness, complements yeast null mutant						
			S511	MEC1, TEL1	CKA2		7, 116, 139, 142, 152, 217, 370, 373, 374, 379
PDA1	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex; catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA; phosphorylated; regulated by glucose; PDH complex is concentrated in spots within the mitochondrial matrix, often near the ERMES complex and near peroxisomes	Y309; S313; S315	S313	PKP1, PKP2	CKA2		7, 32, 56, 100, 110, 122, 139, 142, 152, 217, 258, 331, 370, 374, 379
OM45	Mitochondrial outer membrane protein of unknown function; major constituent of the outer membrane, extending into the intermembrane space; interacts with porin (Por1p) and with Om14p; imported via the presequence pathway involving the TOM and TIM23 complexes, then assembled in the outer membrane by Mim1p; protein abundance increases in response to DNA replication stress	T207	T207		SNF1	PPH22	7, 32, 139, 379
APA1	AP4A phosphorylase; bifunctional diadenosine 5',5'''-P1,P4-tetraphosphate phosphorylase and ADP sulfurylase involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; catalyzes phosphorolysis of dinucleoside oligophosphates, cleaving substrates' alpha/beta-anhydride bond and introducing Pi into the beta-position of the corresponding NDP formed; protein abundance increases under DNA replication stress; APA1 has a paralog, APA2, that arose from the whole genome duplication	T60; T75	T60	KNS1			7, 32, 142, 217, 370, 379

PFK1	Alpha subunit of heterooctameric phosphofructokinase; involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes	S166; S179; S188; S189; S192	S3	MEC1, TEL1		7, 52, 139, 379
PFK2	Beta subunit of heterooctameric phosphofructokinase; involved in glycolysis; indispensable for anaerobic growth; activated by fructose-2,6-bisphosphate and AMP; mutation inhibits glucose induction of cell cycle-related genes	S36; S41; S42; S47; T48; S148; T149; T152; S160; S163; S166; S167; S171; Y172; T173; Y177	S166	SNF1		7, 32, 116, 142, 152, 217, 370, 373, 379
			S167	SNF1		7, 32, 116, 142, 152, 217, 370, 373, 379
			S171	SNF1	CKA2	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S652	PKC1		81
			Y172	SNF1		7, 32, 139
SEC2	Guanyl-nucleotide exchange factor for the small G-protein Sec4p; essential for post-Golgi vesicle transport and for autophagy; associates with the exocyst, via exocyst subunit Sec15p, on secretory vesicles	S632; S740	S515	SNF1		7, 32, 116, 139, 142, 152, 217, 373, 374, 379
CBF1	Basic helix-loop-helix (bHLH) protein; forms homodimer to bind E-box consensus sequence CACGTG present at MET gene promoters and centromere DNA element I (CDEI); affects nucleosome positioning at this motif; associates with other transcription factors such as Met4p and Isw1p to mediate transcriptional activation or repression; associates with kinetochore proteins, required for chromosome segregation;	T138; S140; S149	S45	MEC1, TEL1		7, 52, 116, 142, 152, 370, 373, 379

	protein abundance increases in response to DNA replication stress				
			S48	MEC1, TEL1	7, 32, 52, 116, 142, 152, 370, 373, 379
			S155	SSN3	32, 142, 370, 379
			S156	SSN3	7, 32, 142, 217, 370, 379
			T138	SSN3	7, 32, 139, 142, 217, 379
			T154	CTK1	7, 32, 116, 373, 379
SAC7	GTPase activating protein (GAP) for Rho1p; regulator of a Tor2p-mediated, Rho1p GTPase switch that controls organization of the actin cytoskeleton; negative regulator of the RHO1-PKC1-MAPK cell integrity (CWI) and membrane fluidity homeostasis signaling pathways; potential Cdc28p substrate; SAC7 has a paralog, BAG7, that arose from the whole genome duplication		S16	CDC28	32, 142, 374, 379
			S46	CDC28, CLB2	56, 142, 217, 379
PHO81	Cyclin-dependent kinase (CDK) inhibitor; regulates Pho80p-Pho85p and Pcl7p-Pho85p cyclin-CDK complexes in response to phosphate levels; inhibitory activity for Pho80p-Pho85p requires myo-D-inositol heptakisphosphate (IP7) generated by Vip1p; relative distribution to the nucleus increases upon DNA replication stress	S542; S543	S956	RAD53	7, 52
FPR1	Peptidyl-prolyl cis-trans isomerase (PPIase); binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; N-terminally	S45; S46; S51	S51	PSK2	7, 32, 142, 370, 379

	propionylated in vivo; mutation is functionally complemented by human FKBP1A				
MCK1	Dual-specificity ser/thr and tyrosine protein kinase; roles in chromosome segregation, meiotic entry, genome stability, phosphorylation-dependent protein degradation (Rcn1p and Cdc6p), inhibition of protein kinase A, transcriptional regulation, inhibition of RNA pol III, calcium stress and inhibition of Clb2p-Cdc28p after nuclear division; MCK1 has a paralog, YGK3, that arose from the whole genome duplication	S24; S27; T30; S196; S198; Y199; S202	Y199	MCK1	7, 32, 142, 152, 217, 328, 374, 379
SNF2	Catalytic subunit of the SWI/SNF chromatin remodeling complex; involved in transcriptional regulation; contains DNA-stimulated ATPase activity; functions interdependently in transcriptional activation with Snf5p and Snf6p		S1340	RAD53	7, 370
NPR1	Protein kinase; stabilizes several plasma membrane amino acid transporters by antagonizing their ubiquitin-mediated degradation; phosphorylates Aly2p; negatively regulates Ldb19p-mediated endocytosis through phosphorylation of Ldb19p, which prevents its association with the plasma membrane; Npr1p activity is negatively regulated via phosphorylation by the TOR complex; NPR1 has a paralog, PRR2, that arose from the whole genome duplication	S45; S46; S47; S51	S47	NPR1	105, 142, 374, 379
			S85	TOR1	105
			S90	TOR1	105
			S100	TOR1	7, 105
			S111	TOR1	105
			S116	TOR1	7, 105
			S125	TOR1	105, 142, 217, 379

	S137	TOR1	105, 142, 379
	S141	TOR1	105, 142, 379
	S159	TOR1	105, 142, 370, 379
	S255	TOR1	7, 105, 217, 374
	S257	NPR1	105, 142, 217, 374
	S259	TOR1	105, 142
	S260	TOR1	105, 142, 217, 374, 379
	S288	TOR1	105
	S292	TOR1	105
	S317	TOR1	100, 105, 142, 217, 379
	S320	TOR1	105, 379
	S328	TOR1	105
	S336	TOR1	105
	S338	TOR1	37, 105, 142
	S339	TOR1	105, 142
	S347	TOR1	37, 105
	S349	TOR1	105
	S353	TOR1	32, 105, 142, 217, 374
	S356	TOR1	7, 32, 37, 105, 142, 217, 374
	S357	NPR1	7, 32, 37, 105, 142, 217, 374, 379
	S385	TOR1	105

SIN3	Component of both the Rpd3S and Rpd3L histone deacetylase complexes; involved in transcriptional repression and activation of diverse processes, including mating-type switching and meiosis; involved in the maintenance of chromosomal integrity	T303; T304; T308	S316	CDC28			7, 32, 100, 142, 217, 374, 379
			S1126	MEC1, TEL1			52
			T304	CDC28			7, 32, 142, 217, 374, 379
HSP12	Plasma membrane protein involved in maintaining membrane organization; involved in maintaining organization during stress conditions; induced by heat shock, oxidative stress, osmostress, stationary phase, glucose depletion, oleate and alcohol; protein abundance increased in response to DNA replication stress and dietary restriction; regulated by the HOG and Ras-Pka pathways; required for dietary restriction-induced lifespan extension		S21	MEC1, TEL1		PTC6	7, 32, 52, 56, 116, 142, 370, 373, 379
			S24	PKP1		PTC6	7, 32, 56, 116, 142, 370, 373, 379
			S59	PKP1			7, 32, 116, 142, 370, 373, 379
			S73	PKP1			7, 32, 116, 139, 142, 370, 373, 379
			S87	PKP1			7, 32, 370
			Y25	PKP1			32, 142
SPA2	Component of the polarisome; functions in actin cytoskeletal organization during polarized growth; acts as a scaffold for Mkk1p and Mpk1p cell wall integrity signaling components; potential Cdc28p	S605; S606	S254	CLB2, CDC28	CDC28		7, 32, 56, 116, 122, 139, 142, 217, 373, 374, 379

substrate; coding sequence contains length polymorphisms in different strains; SPA2 has a paralog, SPH1, that arose from the whole genome duplication					
	S274	CLB2, CDC28			7, 32, 116, 142, 373
	S585	CLB2, CDC28		SIW14	7, 32, 56, 116, 122, 139, 142, 152, 217, 370, 373, 379
	S599	CDC28	CDC28		7, 32, 122, 139, 142, 152, 217, 370, 379
	S646	CLB2, CDC28			116, 142, 217, 373
	S883	CDC28			7, 116, 142, 217, 373, 374, 379
	S910	CDC28			7, 116, 142, 217, 370, 373, 374, 379
	S937	CLB2, CDC28			56, 116, 142, 217, 373, 379
	S961	CLB2, CDC28			32, 56, 142, 217, 370, 374, 379
	S979	CLB2, CDC28			7, 32, 142, 217, 370, 379
	S1080	CLB2, CDC28			116, 122, 142, 370, 373, 379
	S1087	CDC28			116, 142, 373, 379

TAF2	TFIID subunit (150 kDa); involved in RNA polymerase II transcription initiation	S318	T19			7, 142, 370
SGV1	Cyclin (Bur2p)-dependent protein kinase; part of the BUR kinase complex which functions in transcriptional regulation; phosphorylates the carboxy-terminal domain (CTD) of Rpo21p and the C-terminal repeat domain of Spt5p; recruits Spt6p to the CTD at the onset of transcription; regulated by Cak1p; similar to metazoan CDK9 proteins	S417	T240	CAK1		7, 56, 100, 139, 142, 152, 379, 442
GSY1	Glycogen synthase; expression induced by glucose limitation, nitrogen starvation, environmental stress, and entry into stationary phase; GSY1 has a paralog, GSY2, that arose from the whole genome duplication; relocalizes from nucleus to cytoplasmic foci upon DNA replication stress	S651; S655	S651	MCK1	RIM11	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S655	MCK1	PHO85	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
MBR1	Protein involved in mitochondrial functions and stress response; overexpression suppresses growth defects of hap2, hap3, and hap4 mutants; MBR1 has a paralog, ISF1, that arose from the whole genome duplication	S222; S224; S226; S227	S69			142
STE11	Signal transducing MEK kinase; involved in pheromone response and pseudohyphal/invasive growth pathways where it phosphorylates Ste7p, and the high osmolarity response pathway, via phosphorylation of Pbs2p; regulated by Ste20p and Ste50p; protein abundance increases in response to DNA replication stress		S281	STE20		86

			S285	STE20		86
			T286	STE20		86
SSD1	Translational repressor with a role in polar growth and wall integrity; regulated by Cbk1p phosphorylation to effect bud-specific translational control and localization of specific mRNAs; interacts with TOR pathway components; contains a functional N-terminal nuclear localization sequence and nucleocytoplasmic shuttling appears to be critical to Ssd1p function	S480; S481; T482; S487; S489; S491; S492; T494	S42	CBK1		156, 217
			S126	CBK1		32, 142, 152, 156
			S152	CBK1		32, 142, 156, 374, 379
			S164	CBK1		32, 56, 142, 156, 217, 370, 374
			S228	CBK1		32, 142, 156
			S231	CDC28		7, 32, 142, 156, 370
			S267	CLB2, CDC28	CDC28	7, 32, 139, 142, 152
			S286	CDC28		7, 32, 142, 152, 156, 374, 379
			S293	CKB1		32, 142, 156
			S319	CKB1		156
			S492	CDC28		7, 32, 100, 116, 142, 217, 370, 373, 374, 379
			T261	CBK1		156
GRR1	F-box protein component of an SCF ubiquitin-ligase complex; modular substrate specificity factor which associates with core SCF (Cdc53p, Skp1p and Hrt1p/Rbx1p) to form the SCF(Grr1) complex; SCF(Grr1)		S199	MPS1		7, 37, 370, 379

	acts as a ubiquitin-protein ligase directing ubiquitination of substrates such as: Gic2p, Mks1p, Mth1p, Cln1p, Cln2p and Cln3p; involved in carbon catabolite repression, glucose-dependent divalent cation transport, glucose transport, morphogenesis, and sulfite detoxification					
			S285	MPS1		37
			S1101	MPS1		37
			T76	MPS1		37
UBP1	Ubiquitin-specific protease; removes ubiquitin from ubiquitinated proteins; cleaves at the C terminus of ubiquitin fusions irrespective of their size; capable of cleaving polyubiquitin chains	S555; S638; S755	S530	CKA1	CKA2	7, 32, 100, 116, 139, 142, 152, 217, 373, 379
			S531	CKA1	CKA2	7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 379
NAP1	Histone chaperone; involved in histone exchange by removing and replacing histone H2A-H2B dimers or histone variant dimers from assembled nucleosomes; involved in the transport of H2A and H2B histones to the nucleus; required for the regulation of microtubule dynamics during mitosis; interacts with mitotic cyclin Clb2p; controls bud morphogenesis; phosphorylated by CK2; protein abundance increases in response to DNA replication stress	T20; T24	S159	CKA1, CKA2, CKB1, CKB2		43
			S177	CKA1, CKA2, CKB1, CKB2	CKA2	7, 32, 37, 43, 116, 139, 142, 152, 217, 370, 373, 379
			S397	CKA1, CKA2,		43

				CKB1, CKB2		
			T20	PTK2		7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
			T24	PTK2		7, 32, 37, 116, 122, 142, 152, 217, 373, 374, 379
FEN1; ELO2	Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; ELO2 has a paralog, ELO1, that arose from the whole genome duplication; lethality of the elo2 elo3 double null mutation is functionally complemented by human ELOVL1 and weakly complemented by human ELOVL3 or ELOV7	T334; S336; S338	S336	MCK1	PHO85	7, 32, 56, 100, 139, 142, 152, 217, 370, 374, 379
			S338	MCK1		7, 32, 56, 100, 142, 152, 217, 370, 374, 379
			T334	MCK1	PHO85	7, 32, 56, 100, 139, 142, 152, 217, 370, 374, 379
RPC53	RNA polymerase III subunit C53	S119; S224; T228; T232; S234	S224	MCK1		7, 32, 56, 116, 142, 152, 204, 217, 370, 373, 374, 379

			T228	MCK1	32, 56, 116, 122, 142, 152, 204, 217, 370, 373, 374, 379
			T232	MCK1	7, 32, 56, 116, 122, 142, 152, 204, 217, 373, 374, 379
BUD3	Guanine nucleotide exchange factor (GEF) for Cdc42p; activates Cdc42p in early G1, accounting for the first stage of biphasic activation, with Cdc24p accounting for the second stage in late G1; involved in the Cdc42p-mediated assembly of the axial landmark that dictates the site for the next round of budding, resulting in the axial budding pattern observed in haploids; localizes with septins to the bud neck contractile ring in mitosis	S1075; S1085	S1501		7, 32, 116, 142, 152, 373, 379
			S1515		7, 142, 379
			S1549		142, 370, 379
			T1440		7, 142, 374
			T1504		7, 32, 142, 152, 379
SRO9	Cytoplasmic RNA-binding protein; shuttles between nucleus and cytoplasm and is exported from the nucleus in an mRNA export-dependent manner; associates with translating ribosomes; involved in heme regulation of Hap1p as a component of the HMC complex, also involved in the organization of actin filaments; contains a La motif; SRO9 has a paralog, SLF1, that arose from the whole genome duplication	S433	S40	CDC28	7, 32, 142, 379

			T69	PSK2			116, 342, 373
			T71	PSK2			342
HSP30	Negative regulator of the H(+)-ATPase Pma1p; stress-responsive protein; hydrophobic plasma membrane localized; induced by heat shock, ethanol treatment, weak organic acid, glucose limitation, and entry into stationary phase	S308; T331	S308		CDC28	SIT4	7, 32, 100, 139, 142, 370, 379
CDC48	AAA ATPase; subunit of polyUb-selective segregase complex involved in ERAD, INM-associated degradation (INMAD), mitotic spindle disassembly, macroautophagy, PMN, ribosome-associated degradation, ribophagy, homotypic ER membrane fusion, SCF complex disassembly, cell wall integrity during heat stress, and telomerase regulation; mobilizes membrane-anchored transcription factors by regulated Ub/proteasome-dependent processing (RUP); human ortholog VCP complements a cdc48 mutant	S770	S770	MPS1			7, 32, 37, 56, 142, 217, 370, 374, 379
			T735	MPS1			7, 37, 139, 142, 370, 379
PPZ1	Serine/threonine protein phosphatase Z, isoform of Ppz2p; involved in regulation of potassium transport, which affects osmotic stability, cell cycle progression, and halotolerance		S49			OCA1	32, 142, 217, 379
			S142	CDC28			142, 217, 379
			S265	CLB2, CDC28			142, 217, 379
			T261	CLB2, CDC28			142, 217, 379
CDC60	Cytosolic leucyl tRNA synthetase; ligates leucine to the appropriate tRNA; human homolog LARS can complement yeast	T142; T152	T142	CDC28			116, 142, 373

	temperature-sensitive mutant at restrictive temperature					
RFA2	Subunit of heterotrimeric Replication Protein A (RPA); RPA is a highly conserved single-stranded DNA binding protein involved in DNA replication, repair, and recombination; RPA protects against inappropriate telomere recombination, and upon telomere uncapping, prevents cell proliferation by a checkpoint-independent pathway; in concert with Sgs1p-Top2p-Rmi1p, stimulates DNA catenation/decatenation activity of Top3p; protein abundance increases in response to DNA replication s		S27	IME2		7, 62, 345
			S122	IME2		7, 25, 52, 56, 113, 116, 122, 139, 142, 217, 373, 374, 379
GSY2	Glycogen synthase; expression induced by glucose limitation, nitrogen starvation, heat shock, and stationary phase; activity regulated by cAMP-dependent, Snf1p and Pho85p kinases as well as by the Gac1p-Glc7p phosphatase; GSY2 has a paralog, GSY1, that arose from the whole genome duplication; relocalizes from cytoplasm to plasma membrane upon DNA replication stress	S651; S655	S651	MCK1	RIM11	7, 32, 37, 100, 122, 133, 139, 142, 148, 149, 152, 217, 342, 370, 374, 379, 427
			S655	PCL10, PHO85		7, 26, 37, 100, 122, 133, 142, 148, 149, 217, 342, 370, 374, 379, 427

			T668	PCL10, PHO85	26, 133, 148, 149, 427
SPT5	Spt4p/5p (DSIF) transcription elongation factor complex subunit; the Spt4/5 complex binds to ssRNA in a sequence-specific manner, and in concert with RNAP I and II has multiple roles regulating transcriptional elongation, RNA processing, quality control, and transcription-coupled repair; interacts with DNA upstream of RNAPII and the non-template strand of the transcription bubble; Spt5p is the only transcription elongation factor conserved in all domains of life	T40	S931	BUR2, SGV1	227
			S937	BUR2, SGV1	227
			S948	BUR2, SGV1	227
			S958	BUR2, SGV1	227
			S969	BUR2, SGV1	227
			S975	BUR2, SGV1	227
			S981	BUR2, SGV1	227
			S987	BUR2, SGV1	227
			S1000	BUR2, SGV1	227
			S1009	BUR2, SGV1	227, 379
			S1015	BUR2, SGV1	142, 227, 379
			S1032	BUR2, SGV1	142, 152, 227, 379
			S1043	BUR2, SGV1	152, 227, 379
			S1052	BUR2, SGV1	142, 227, 379

			S1058	BUR2, SGV1		152, 227, 379
MIG1	Transcription factor involved in glucose repression; sequence specific DNA binding protein containing two Cys2His2 zinc finger motifs; regulated by the SNF1 kinase and the GLC7 phosphatase; regulates filamentous growth along with Mig2p in response to glucose depletion; activated in stochastic pulses of nuclear localization, shuttling between cytosol and nucleus depending on external glucose levels and its phosphorylation state	S278	S222	SNF1		32, 77, 142, 152, 367, 428
			S264	CLB2, CDC28		32, 142, 152, 379
			S278	SNF1		7, 32, 77, 142, 152, 299, 367, 379, 396, 428
			S311	SNF1		6, 7, 77, 122, 142, 152, 217, 299, 307, 370, 379, 396, 428
			S381	SNF1		7, 77, 142, 367, 428
FUN19	Non-essential protein of unknown function; expression induced in response to heat stress; FUN19 has a paralog, YOR338W, that arose from the whole genome duplication	T194; S207; S267; S269	S207	CDC28	PHO85	7, 139, 142
			S211	CDC28		7, 142
GAC1	Regulatory subunit for Glc7p type-1 protein phosphatase (PP1); tethers Glc7p to Gsy2p glycogen synthase, binds Hsf1p heat shock transcription factor, required for induction of some HSF-regulated genes under heat		S66	CLB2, CDC28		142, 379

	shock; GAC1 has a paralog, PIG1, that arose from the whole genome duplication					
BMH1	14-3-3 protein, major isoform; controls proteome at post-transcriptional level, binds proteins and DNA, involved in regulation of exocytosis, vesicle transport, Ras/MAPK and rapamycin-sensitive signaling, aggresome formation, spindle position checkpoint; protein increases in abundance and relative distribution to the nucleus increases upon DNA replication stress; antiapoptotic gene similar to human 14-3-3; BMH1 has a paralog, BMH2, that arose from whole genome duplication	T231; T234; S235; S238; S240	S238	HRR25		32, 63, 142, 374, 417
BEM1	Protein containing SH3-domains; involved in establishing cell polarity and morphogenesis; functions as a scaffold protein for complexes that include Cdc24p, Ste5p, Ste20p, and Rsr1p	S458	S72			7, 32, 131, 370, 379, 401
			S458		SNF1	7, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
MCM2	Protein involved in DNA replication; component of the Mcm2-7 hexameric helicase complex that binds chromatin as a part of the pre-replicative complex; relative distribution to the nucleus increases upon DNA replication stress	T547	S107	CDC7		323
			S164	CDC7		39, 142, 310, 311, 323, 376
			S170	CDC7		39, 142, 310, 311, 323, 376
NTH1	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses;	S83	S20	TPK1		7, 100, 104, 122, 142,

	phosphorylated and activated by Cdc28p at the G1/S phase transition to coordinately regulate carbohydrate metabolism and the cell cycle; inhibited by Dcs1p; NTH1 has a paralog, NTH2, that arose from the whole genome duplication				217, 370, 379, 423
			S66	CDC28	7, 32, 56, 100, 104, 142, 152, 370, 374, 379, 423
			S83	TPK1	7, 32, 56, 100, 104, 142, 152, 370, 374, 379, 423
IRE1	Serine-threonine kinase and endoribonuclease; transmembrane protein that mediates the unfolded protein response (UPR) by regulating Hac1p synthesis through HAC1 mRNA splicing; role in homeostatic adaptation to ER stress; Kar2p binds inactive Ire1p and releases from it upon ER stress	S604; S618	S840		9, 123, 356, 379
			S841		9, 37, 123, 356, 379
PUP2	Alpha 5 subunit of the 20S proteasome; involved in ubiquitin-dependent catabolism; human homolog is subunit zeta	T55; S56; S251	S56	CDC28	7, 122, 142, 181, 217, 370, 374, 379
SPC110	Inner plaque spindle pole body (SPB) component; ortholog of human kendrin; gamma-tubulin small complex (gamma-TuSC) receptor that interacts with Spc98p to recruit the complex to the nuclear side of the SPB, connecting nuclear microtubules to the SPB; promotes gamma-TuSC assembly and oligomerization to initiate microtubule nucleation; interacts with Tub4p-complex		S36	CDC28	7, 37, 103, 153, 189, 224, 370, 379

	and calmodulin; phosphorylated by Mps1p in cell cycle-dependent manner					
			S60	MPS1		7, 32, 103, 142, 152, 153, 217, 224, 374, 379
			S72	MPS1		37, 142
			S91	CDC28		7, 116, 139, 142, 153, 221, 224, 373, 379
			T64	MPS1		103, 153, 224
			T68	MPS1		103, 153, 224
CDC3	Component of the septin ring that is required for cytokinesis; septins are GTP-binding proteins that assemble with other septins into rod-like complexes that can associate with other rods to form filament polymers; septin rings at the mother-bud neck act as scaffolds for recruiting factors needed for cell division and as barriers to prevent diffusion of specific proteins between mother and daughter cells	S2; S9	S498	CTK1		32, 379
			S503	CLB2, CDC28		32, 116, 122, 142, 152, 373, 374, 379, 389
			S509	CLB2, CDC28		7, 32, 37, 116, 142, 152, 217, 373, 374, 379, 389
HOG1	Mitogen-activated protein kinase involved in osmoregulation; controls global reallocation of RNAPII during osmotic shock; mediates recruitment/activation of RNAPII at Hot1p-	Y176; T179	T174	PBS2	PTC2, PTC3	18, 30, 32, 37, 100, 152, 241,

	dependent promoters; binds calmodulin; stimulates antisense transcription to activate CDC28; defines novel S-phase checkpoint with Mrc1p that prevent replication/transcription conflicts; nuclear form represses pseudohyphal growth; autophosphorylates; protein abundance increases under DNA replication stress					352, 379, 408, 420
			Y176	PBS2	PTC1	7, 18, 30, 32, 100, 139, 142, 152, 241, 352, 379, 408, 420
NIP1	eIF3c subunit of the eukaryotic translation initiation factor 3 (eIF3); involved in the assembly of preinitiation complex and start codon selection; eIF3 is also involved in programmed stop codon readthrough	S98; S99; S103; S222; T228; T239	S98	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
			S99	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
			S103	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
NUP2	Nucleoporin involved in nucleocytoplasmic transport; binds to either the nucleoplasmic or cytoplasmic faces of the nuclear pore complex depending on Ran-GTP levels; also has a role in chromatin organization	T14; S17; S20; S84; S203; S205; S537; S538; S540; T577; S581	S17	MCK1		7, 32, 56, 100, 116, 142, 152, 217, 369, 373, 374, 379
			S20	MCK1		7, 32, 56, 100, 116, 142, 152, 217, 369,

						373, 374, 379
			S68	RAD53		7, 139, 142, 370
			S203	RAD53	PTP1	7, 32, 56, 116, 142, 152, 217, 370, 373, 374
			S205	ALK2	PTP1	7, 32, 56, 116, 142, 152, 217, 370, 373, 374
			S248	RAD53		7, 370
			S284	RAD53		7, 370
			S317	RAD53		7, 370
			S351	RAD53		7, 52, 370
			S368	RAD53		7, 142, 370, 379
			S399	MEC1, TEL1		370, 379
			S512	RAD53		370
			S523	RAD53		370
PAN1	Part of actin cytoskeleton-regulatory complex Pan1p-Sla1p-End3p; associates with actin patches on cell cortex; promotes protein-protein interactions essential for endocytosis; binds to and activates Arp2/3 complex in vitro; phosphorylation of Thr-1225 is regulated by MAPK Hog1p in response to osmotic stress; previously thought to be a subunit of poly(A) ribonuclease	T570; T993; S1003; S1250; S1253; S1255; T1256	T148	PRK1		147, 395, 453
			T170	PRK1		147, 395, 453
			T194	PRK1		147, 395, 453
			T221	PRK1		395, 453

			T241	PRK1	7, 147, 395, 453
			T398	PRK1	147, 395, 453
			T415	PRK1	147, 395, 453
			T428	PRK1	147, 395, 453
			T452	PRK1	147, 395, 453
			T473	PRK1	147, 395, 453
			T504	PRK1	147, 395, 453
			T513	PRK1	147, 395, 453
			T544	PRK1	147, 395, 453
			T551	PRK1	147, 395, 453
			T566	PRK1	7, 146
			T570	PRK1	7, 32, 142, 147, 152, 379, 395, 453
PAH1	Mg2+-dependent phosphatidate (PA) phosphatase; dephosphorylates PA to yield diacylglycerol; regulates phospholipid synthesis, nuclear/ER membrane growth, lipid droplet formation, triacylglycerol synthesis, vacuolar homeostasis and cell wall integrity; phosphorylated by Pho85p/Pho80p, Cdc28p/Cyclin B, PKA, PKC, and CKII, regulating activity, localization, and proteosomal degradation; homolog of mammalian lipins 1 and 2; human homologs LPIN1, LPIN2, LPIN3 complement the null	T163; T164; S166; T170; T175; T176; S814	S110	NEM1, SPO7	58, 60, 289
			S114	NEM1, SPO7	58, 60, 289

			S168			NEM1, SPO7	58, 60, 116, 289, 373, 379
			S602	CDC28		NEM1, SPO7	7, 58, 60, 142, 217, 289, 379
			S744			NEM1, SPO7	7, 58, 60, 116, 142, 152, 217, 289, 373, 374, 379
			S748			NEM1, SPO7	7, 58, 60, 116, 122, 142, 152, 217, 289, 373, 374, 379
			T723			NEM1, SPO7	58, 60, 289
SIP1	Alternate beta-subunit of the Snf1p kinase complex; may confer substrate specificity; vacuolar protein containing KIS (Kinase-Interacting Sequence) and ASC (Association with Snf1 kinase Complex) domains involved in protein interactions	S331	S198	CDC28			142, 217, 379
			S200	CDC28			7, 116, 142, 217, 373, 374, 379
SRP40	Nucleolar serine-rich protein; role in preribosome assembly or transport; may function as a chaperone of small nucleolar ribonucleoprotein particles (snoRNPs); immunologically and structurally to rat Nopp140	S133; T141	S133			SIW14	32, 56, 116, 152, 373
STH1	ATPase component of the RSC chromatin remodeling complex; required for expression of early meiotic genes; promotes base excision repair in chromatin; essential helicase-related protein homologous to Snf2p	S51; S52; S1188	S1172	MEC1, TEL1	CKA2		7, 52

			T1166	MEC1, TEL1	CKA2		7, 52, 139
YEL043W	Predicted cytoskeleton protein involved in intracellular signaling; based on quantitative analysis of protein-protein interaction maps; may interact with ribosomes, based on co-purification studies; contains fibronectin type III domain fold	S524	S847	CDC28			142
			S862	CDC28			142
SLA1	Cytoskeletal protein binding protein; required for assembly of the cortical actin cytoskeleton; interacts with proteins regulating actin dynamics and proteins required for endocytosis; found in the nucleus and cell cortex; has 3 SH3 domains	S794; T797; S799; T831; T834; T835	S437	CLB2, CDC28			7, 32, 142, 152, 370, 374, 379
			S449			PSR2	7, 32, 116, 142, 217, 373, 379
YSC84	Actin-binding protein; involved in bundling of actin filaments and endocytosis of actin cortical patches; activity stimulated by Las17p; contains SH3 domain similar to Rvs167p; YSC84 has a paralog, LSB3, that arose from the whole genome duplication	Y296; S301	S311				7, 32, 142, 217, 374, 379
UGP1	UDP-glucose pyrophosphorylase (UGPase); catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; involved in PKA-mediated oxidative stress resistance and long-term survival in stationary phase; UGP1 has a paralog, YHL012W, that arose from the whole genome duplication		S11	PSK2			7, 32, 37, 56, 100, 116, 122, 142, 217, 342, 368, 373, 374, 379
CBF5	Pseudouridine synthase catalytic subunit of box H/ACA snoRNPs; acts on large and small rRNAs, on snRNA U2, and on some mRNAs; mutations in human ortholog dyskerin cause the disorder dyskeratosis	T378; S398	S395	MEC1, TEL1			32, 52, 116, 139, 142, 373, 374, 379

	congenita; small nucleolar ribonucleoprotein particles are also known as snoRNPs				
			S399	MEC1, TEL1	7, 32, 52, 116, 142, 370, 373, 374, 379
			T396	FRK1	7, 32, 139
PPZ2	Serine/threonine protein phosphatase Z, isoform of Ppz1p; involved in regulation of potassium transport, which affects osmotic stability, cell cycle progression, and halotolerance	T298; S299; S310; S314; S315; S317; S359; S362	S299	CLB2, CDC28	7, 142, 374, 379
			S310	CLB2, CDC28	7, 37, 116, 142, 373, 374, 379
SLA2	Adaptor protein that links actin to clathrin and endocytosis; involved in membrane cytoskeleton assembly and cell polarization; present in the actin cortical patch of the emerging bud tip; dimer in vivo		S308	CDC28	7, 32, 100, 142, 152, 217, 374, 379
			T290	SSK2	7, 32, 142, 217, 370, 374, 379
			T294	CDC28	7, 32, 100, 122, 142, 217, 370, 374, 379
			T296	CDC28	7, 32, 100, 122, 142, 217, 370, 374, 379
			T298	CDC28	7, 32, 100, 142, 152, 217, 370, 374, 379
PGM1	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; PGM1 has	T111; T118; S120; S513	S120	FRK1	7, 32, 116, 122, 142, 152, 217, 370, 373, 374, 379

	a paralog, PGM2, that arose from the whole genome duplication					
TRM2	tRNA methyltransferase; 5-methylates the uridine residue at position 54 of tRNAs and may also have a role in tRNA stabilization or maturation; endo-exonuclease with a role in DNA repair	S93	S92	KNS1		32, 116, 139, 142, 152, 217, 373, 374, 379
			S93	KNS1		7, 32, 56, 142, 152, 217, 370, 374, 379
MKS1	Pleiotropic negative transcriptional regulator; involved in Ras-CAMP and lysine biosynthetic pathways and nitrogen regulation; involved in retrograde (RTG) mitochondria-to-nucleus signaling	S440; S442	S217	FRK1		7, 32
TGL1	Steryl ester hydrolase; one of three gene products (Yeh1p, Yeh2p, Tgl1p) responsible for steryl ester hydrolase activity and involved in sterol homeostasis; localized to lipid particle membranes	S462; S466; S538	S466	CDC28		142, 379
			S492	TPK3		7, 32, 142, 370, 374, 379
EDE1	Scaffold protein involved in the formation of early endocytic sites; putative regulator of cytokinesis; homo-oligomerization is required for localization to and organization of endocytic sites; has a network of interactions with other endocytic proteins; binds membranes in a ubiquitin-dependent manner; may also bind ubiquitinated membrane-associated proteins; interacts with Cmk2 and functions upstream of CMK2 in regulating non-apoptotic cell death; homolog of mammalian Eps15	S241; S931; S1006; S1008; S1011; S1012; T1065; S1093; S1095; S1096; S1100; S1104; T1160; T1178; S1179; S1181; S1187; T1307; S1309	S241		PTC4	7, 32, 100, 122, 142, 152, 217, 370, 374, 379
			S244		PTC4	7, 32, 100, 122, 142, 152, 217, 374, 379

			S249		PTC4	7, 32, 142, 152, 217, 374, 379
			S527		PSR2	32, 152, 370
			S1069		CMP2	7, 32, 142, 379
			S1096	FUS3		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			S1100	PHO85		7, 32, 56, 100, 116, 142, 152, 217, 370, 373, 374, 379
			T238	CDC28		7, 142, 217, 379
			T1072		CMP2	7, 32, 142, 379
PIN4	Protein involved in G2/M phase progression and response to DNA damage; interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage	T512; S538; S541; S545; S653; S655	S466	CDC28		7, 32, 116, 122, 139, 142, 217, 373, 374, 379
			S541	CDC28		32, 122, 142, 152, 379
			S653		SIT4	7, 32, 37, 116, 122, 142, 370, 373, 374, 379
			S655		SIT4	7, 32, 116, 122, 142, 370, 373, 374, 379

SHP1	UBX domain-containing substrate adaptor for Cdc48p; ubiquitin regulatory X domain-containing protein that acts as a substrate recruiting cofactor for Cdc48p; positively regulates Glc7p PPase activity to promote growth and mitotic progression in complex with Cdc48p; ubiquitinated protein interactor involved in ER-associated degradation (ERAD); regulated by nuclear Ub-dependent degradation (INMAD pathway) independent of the Asi and Doa10 complexes; homolog of human p47 (NSFL1C)	S97; S106; T107; S115; S224; S315; S321; S322; T331	S106	KNS1		7, 32, 100, 116, 152, 373, 379
			S108	PTK1		7, 32, 100, 116, 152, 370, 373, 379
			S315	CDC28	CDC28	7, 32, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S322	CDC28		7, 32, 139, 142, 217, 374, 379
SEG2; YKL105C	Eisosome component; likely plays only a minor role in eisosome assembly; shown to interact with Seg1p by affinity purification and mass spec; SWAT-GFP and mCherry fusion proteins localize to the cell periphery; similar to A. gossypii SEG gene which is important for stabilizing eisosomes; SEG2 has a paralog, SEG1, that arose from the whole genome duplication	S524	S187	SNF1		7, 32, 139, 142, 374, 379
			S980	CDC28		142, 379
FAB1	1-phosphatidylinositol-3-phosphate 5-kinase; vacuolar membrane kinase that generates phosphatidylinositol (3,5)P2,	S1710; S1712	T183			7, 142, 370

	which is involved in vacuolar sorting and homeostasis				
TSA1	Thioredoxin peroxidase; acts as both ribosome-associated and free cytoplasmic antioxidant; self-associates to form high-molecular weight chaperone complex under oxidative stress; chaperone activity essential for growth in zinc deficiency; required for telomere length maintenance; binds and modulates Cdc19p activity; protein abundance increases, forms cytoplasmic foci during DNA replication stress; TSA1 has a paralog, TSA2, that arose from the whole genome duplication	T167; T174; T179; T183; S187	T174	FRK1	7, 32, 116, 142, 373, 379
GCS1	ADP-ribosylation factor GTPase activating protein (ARF GAP); involved in ER-Golgi transport; required for prospore membrane formation; regulates phospholipase Spo14p; shares functional similarity with Glo3p; GCS1 has a paralog, SPS18, that arose from the whole genome duplication	S149; T151; S157; T161; S168; T170	S157	CKA1	7, 32, 142, 217, 370, 374, 379
			T151	MCK1	32, 142, 152, 217
			T161	CDC28	7, 32, 139, 142, 217, 370, 374, 379
			T170	CLB2, CDC28	7, 32, 100, 142, 370, 379
DEF1	RNAPII degradation factor; forms a complex with Rad26p in chromatin, enables ubiquitination and proteolysis of RNAPII present in an elongation complex; mutant is deficient in Zip1p loading onto chromosomes during meiosis	T258; S260; S307	S273	RAD53	56, 116, 370
BDF1	Protein involved in transcription initiation; functions at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains;	S270; S612; S613; S615; T617	S630	MEC1, TEL1	52, 379

	corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p; BDF1 has a paralog, BDF2, that arose from the whole genome duplication						
SWH1	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats and FFAT motif; interacts with ER anchor Scs2p at the nucleus-vacuole junction; regulated by sterol binding; SWH1 has a paralog, OSH2, that arose from the whole genome duplication	T432; S442; T443; S488; S490; S492; S678; S683; T694; S732; T1053; S1056	S1056	SNF1	SNF1		7, 32, 139, 142, 370, 379
			T1053	SNF1	SNF1		7, 32, 139, 370, 379
KKQ8	Putative serine/threonine protein kinase with unknown cellular role; KKQ8 has a paralog, HAL5, that arose from the whole genome duplication	S344; S347	S21				7, 37, 122, 142, 374, 379
SIS2	Negative regulatory subunit of protein phosphatase 1 (Ppz1p); involved in coenzyme A biosynthesis; subunit of phosphopantothenoylcysteine decarboxylase (PPCDC: Cab3p, Sis2p, Vhs3p) complex and the CoA-Synthesizing Protein Complex (CoA-SPC: Cab2p, Cab3p, Cab4p, Cab5p, Sis2p and Vhs3p); SIS2 has a paralog, VHS3, that arose from the whole genome duplication	T119; S121; S124; S130; S132	S47	CDC28			7, 32, 142, 217, 370, 374, 379
			S56	CDC28			7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
EAP1	eIF4E-associated protein, competes with eIF4G for binding to eIF4E; accelerates mRNA degradation by promoting decapping, facilitated by interaction with eIF4E; essential for Puf5p mediated repression; associates with Puf5p and Dhh1p; inhibits cap-dependent translation;	S389; S390; T391	S363			PSR1	32, 142

	functions independently of eIF4E to maintain genetic stability; plays a role in cell growth, implicated in the TOR signaling cascade						
			S387	MCK1			7, 32
ELF1	Transcription elongation factor with a conserved zinc finger domain; implicated in the maintenance of proper chromatin structure in actively transcribed regions; deletion inhibits Brome mosaic virus (BMV) gene expression	S124; S142	S117	PSK2			7, 32, 116, 142, 193, 217, 370, 373, 374, 379
			S124	PSK2			7, 32, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
TTI1	Subunit of the ASTRA complex, involved in chromatin remodeling; telomere length regulator involved in the stability or biogenesis of PIKKs such as TORC1; similar to S. pombe Tti1p; detected in highly purified mitochondria in high-throughput studies	S817	S817			PPH22	7, 32, 116, 142, 370, 373, 374
YKR018C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; protein abundance increases in response to DNA replication stress; YKR018C has a paralog, IML2, that arose from the whole genome duplication	T184; S185; S187; S192; T193; T196; T199; S246; S375; S377; S380	S380	PKH2			7, 32, 116, 142, 152, 217, 370, 373, 374, 379
GPT2	Glycerol-3-phosphate/dihydroxyacetone phosphate sn-1 acyltransferase; located in lipid particles and the ER; involved in the stepwise acylation of glycerol-3-phosphate and dihydroxyacetone in lipid biosynthesis; the most conserved motifs and functionally relevant residues are oriented towards the ER lumen	S631; S632; S668; S671; T692; S693	T692	YPK1	CKA2		7, 32, 122, 139, 142, 370, 374, 379

PGM2	Phosphoglucomutase; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; functions as the acceptor for a Glc-phosphotransferase; protein abundance increases in response to DNA replication stress; PGM2 has a paralog, PGM1, that arose from the whole genome duplication	T111; T117; S119; S512	S119	RAD53		7, 32, 116, 122, 142, 370, 373, 374, 379
STV1	Subunit a of the vacuolar-ATPase V0 domain; one of two isoforms (Stv1p and Vph1p); Stv1p is located in V-ATPase complexes of the Golgi and endosomes while Vph1p is located in V-ATPase complexes of the vacuole	S223; S228	S223	CTK1		7, 32, 122, 142, 152, 217, 370, 374, 379
YRO2	Protein with a putative role in response to acid stress; null mutant is sensitive to acetic acid; transcription is regulated by Haa1p and induced in the presence of acetic acid; protein observed in plasma membrane foci in the presence of acetic acid; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies	T341; S343	S297		SIW14	32
			S299		SIW14	7, 32, 142, 370, 379
AKL1	Ser-Thr protein kinase; member (with Ark1p and Prk1p) of the Ark kinase family; involved in endocytosis and actin cytoskeleton organization	S407; S504; S541	S504	CLB2, CDC28		7, 32, 56, 139, 142, 152, 374, 379
			S801	CLB2, CDC28		7, 37, 116, 142, 217, 373, 379
			S1072	AKL1		7, 32, 34, 142, 152, 217, 338, 370, 374, 379
BAP2	High-affinity leucine permease; functions as a branched-chain amino acid permease	S16; S24	S16	CDC28		7, 142, 370, 374, 379

	involved in uptake of leucine, isoleucine and valine; contains 12 predicted transmembrane domains; BAP2 has a paralog, BAP3, that arose from the whole genome duplication					
ISW1	ATPase subunit of imitation-switch (ISWI) class chromatin remodelers; with Ioc3p forms Isw1a complex involved in repression of transcription initiation; with Ioc2p and Ioc4p forms Isw1b complex involved in regulation of transcription elongation; Isw1b recruited to ORFs by H3K36 methylation and acts with Chd1p to prevent trans-histone exchange over coding regions; Isw1p import into nucleus depends on C-terminal bipartite nuclear targeting signal KRIR X19 KKAK		T694	CDC28		7, 116, 142, 370, 373, 379
RTG3	bHLH/Zip transcription factor for retrograde (RTG) and TOR pathways; forms a complex with another bHLH/Zip protein, Rtg1p, to activate the pathways; target of Hog1p		S371		CMP2	32
ECM21	Protein involved in regulating endocytosis of plasma membrane proteins; identified as a substrate for ubiquitination by Rsp5p and deubiquitination by Ubp2p; promoter contains several Gcn4p binding elements; ECM21 has a paralog, CSR2, that arose from the whole genome duplication	S18; T20; S136; S140; S306; T959; S962; S1027; T1028; S1030	S33	CLB2, CDC28		32, 116, 142, 373, 379
			S550	DUN1		7, 52
			S1030	CDC28		7, 142, 152, 308, 379
			T1028	CDC28		7, 142, 152, 379
HEK2	RNA binding protein involved in asymmetric localization of ASH1 mRNA; represses translation of ASH1 mRNA, an effect reversed by Yck1p-dependent phosphoryation; regulates telomere position effect and length; similarity to hnRNP-K	S252; S358; S360; S362	S252		YVH1	7, 32, 301, 370, 374, 379
			S358	YCK1		7, 56, 142, 217, 301, 370, 374

			S360	YCK1	7, 142, 217, 301, 370, 374
			S362	YCK1	7, 142, 301, 370, 379
			S381	YCK1	301
			T352	YCK1	301
			T355	YCK1	301
NCL1	S-adenosyl-L-methionine-dependent tRNA: m5C-methyltransferase; methylates cytosine to m5C at several positions in tRNAs and intron-containing pre-tRNAs; increases proportion of tRNALeu(CAA) with m5C at wobble position in response to hydrogen peroxide, causing selective translation of mRNA from genes enriched in TTG codon; loss of NCL1 confers hypersensitivity to oxidative stress; similar to Nop2p and human proliferation associated nucleolar protein p120	T415; S423; S424; S431; T664; T665; S667; T671; T673; T675; S676; T677	S424	MKK2	7, 32, 116, 142, 373, 374, 379
			T426	CDC28	7, 32, 142, 379
IST2	Cortical ER protein involved in ER-plasma membrane tethering; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to the plasma membrane (PM) and regulate PM phosphatidylinositol-4-phosphate (PI4P) levels by controlling access of Sac1p phosphatase to its substrate PI4P in the PM; localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process	T701; S704; T712; S714; T726; S729; Y730; T736; S757; S763; S764; S767; S768; S844; S847; T850; T853	S764	CTK1	32, 374
			S767	YPK1	7, 32, 374, 379
EXO84	Exocyst subunit with dual roles in exocytosis and spliceosome assembly; subunit of the the exocyst complex which mediates polarized targeting and tethering of	T28; S31	S31		142, 370, 379

	post-Golgi secretory vesicles to active sites of exocytosis at the plasma membrane (PM) prior to SNARE-mediated fusion; required for exocyst assembly and targeting the complex to specific sites on the bud tip PM; associates the U1 snRNP; role in pre-mRNA splicing and prespliceosome formation; possible Cdc28 substrate				
			T28		142, 370
SDS24	Protein involved in cell separation during budding; one of two S. cerevisiae homologs (Sds23p and Sds24p) of the S. pombe Sds23 protein, which is implicated in APC/cyclosome regulation; may play an indirect role in fluid-phase endocytosis; protein abundance increases in response to DNA replication stress; SDS24 has a paralog, SDS23, that arose from the whole genome duplication	T90; T92; S94; S98; S404; T441; S447; S458	S94	CTK1	7, 32, 56, 116, 142, 373, 379
			S458	CDC28	7, 142, 217, 370, 374, 379
TPS3	Regulatory subunit of trehalose-6-phosphate synthase/phosphatase; involved in synthesis of storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway; TPS3 has a paralog, TSL1, that arose from the whole genome duplication	S51; S52; T55; S56; S58; S59; Y61; S148; S150; S154; S181; S195	S148	CDC28	7, 32, 122, 142, 152, 217, 374, 379
TSL1	Large subunit of trehalose 6-phosphate synthase/phosphatase complex; Tps1p-Tps2p complex converts uridine-5'-diphosphoglucose and glucose 6-phosphate to trehalose; contributes to survival to acute lethal heat stress; mutant has aneuploidy tolerance; protein abundance increases in response to DNA replication stress; TSL1 has a paralog, TPS3, that arose from the whole genome duplication	S49; S53; S56; S71; S73; S77; S79; S85; S86; T87; T88; T115; S118; S135; S137; S138; S147; S155; S157; S161; S186; T191; S192; T194; S195; T205; T215; S216; T219; S220	S49	CKA1	7, 32, 122, 142, 379

			S77	CDC28	CDC28		7, 32, 100, 122, 139, 142, 370, 374, 379
			S79	MCK1			7, 32, 142, 370
			S135	CDC28	CDC28		7, 32, 139, 142, 370, 374
			S147	CDC28	CDC28		7, 32, 139, 142, 370, 374, 379
			S155	MCK1			32, 142
			S157	MCK1			32
			S161	CDC28	CDC28		7, 32, 122, 139, 142, 374, 379
LEO1	Component of the Paf1 complex; which associates with RNA polymerase II and is involved in histone methylation; plays a role in regulating Ty1 transposition; involved in transcription elongation as demonstrated by the G-less-based run-on (GLRO) assay	S132; S358; S372; T374	S34	MEC1, TEL1			370
			S132			CMP2	7, 32, 116, 142, 217, 373, 379
			S339	MEC1, TEL1			52, 370, 379
RCK2	Protein kinase involved in response to oxidative and osmotic stress; identified as suppressor of S. pombe cell cycle checkpoint mutations; similar to CaM (calmodulin) kinases; RCK2 has a paralog, RCK1, that arose from the whole genome duplication	S186; S187	S46	CDC28			7, 32, 56, 116, 122, 142, 152, 370, 373, 374, 379
			S520	HOG1			31, 159, 391
			T379	HOG1			391
RFC1	Subunit of heteropentameric Replication factor C (RF-C); RF-C is a DNA binding protein and ATPase that acts as a clamp	S40; S79; S80; T82; S88	T48	CLB2, CDC28			142, 379

	loader of the proliferating cell nuclear antigen (PCNA) processivity factor for DNA polymerases delta and epsilon				
SIC1	Cyclin-dependent kinase inhibitor (CKI); inhibitor of Cdc28-Clb kinase complexes that controls G1/S phase transition, preventing premature S phase and ensuring genomic integrity; phosphorylated by Clb5/6-Cdk1 and Cln1/2-Cdk1 kinase which regulate timing of Sic1p degradation; phosphorylation targets Sic1p for SCF(CDC4)-dependent turnover; functional homolog of mammalian Kip1	S191	S69		33, 188, 262, 283, 287, 295, 414
			S76		33, 188, 261, 262, 283, 287, 295, 414, 441
			S80		37, 188, 262, 283, 414
			S145		37, 97, 122, 283, 295, 354, 414
			S191		7, 32, 37, 116, 122, 139, 142, 152, 272, 283, 373, 374, 414
			S201		7, 23, 37, 61, 64, 65, 116, 139, 142, 217, 374, 379
			T2	CDC28	33, 139, 283, 287, 295, 414
			T5		7, 139, 283, 287, 414

			T33			37, 97, 262, 283, 287, 354, 413, 414
			T45			37, 97, 262, 354, 379
			T48			33, 261, 262, 283, 295, 354, 414
			T173			7, 32, 90, 97, 116, 122, 152, 217, 272, 273, 283, 295, 373, 414, 461
KIC1	Protein kinase of the PAK/Ste20 family, required for cell integrity; physically interacts with Cdc31p (centrin), which is a component of the spindle pole body; part of the RAM network that regulates cellular polarity and morphogenesis		S735	CLB2, CDC28		7, 142, 374, 379
CIC1	Essential protein that interacts with proteasome components; has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles	S365; S366	S5	MCK1		32, 100, 370
			S7	MCK1		32, 100, 370
			S10	MCK1		7, 32, 100, 116, 370, 373
			S17	MCK1	PSR1	32, 116, 370, 373, 379
			T11	MCK1	PSR1	7, 32, 100, 116, 370, 373, 379
			T15	MCK1		32, 116, 373, 379

RSC30	Component of the RSC chromatin remodeling complex; non-essential gene required for regulation of ribosomal protein genes and the cell wall/stress response; null mutants are osmosensitive; RSC30 has a paralog, RSC3, that arose from the whole genome duplication	S150; S152	S815	MEC1, TEL1			52
YHR097C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus; YHR097C has a paralog, PAL1, that arose from the whole genome duplication	S221; S222; T223; T224; T225; S233	S222			YVH1	7, 32, 100, 116, 217, 370, 373, 379
			S315	PTK1			7, 32, 56, 116, 142, 152, 373, 379
			T313			PPQ1	7, 32, 116, 142, 152, 373, 379
BZZ1	SH3 domain protein implicated in regulating actin polymerization; able to recruit actin polymerization machinery through its SH3 domains; colocalizes with cortical actin patches and Las17p; interacts with type I myosins	S472	S472	SNF1			7, 32, 142, 374, 379
KEL1	Protein required for proper cell fusion and cell morphology; forms a complex with Bud14p and Kel2p that regulates Bnr1p (formin) to affect actin cable assembly, cytokinesis, and polarized growth; functions in a complex with Kel2p to negatively regulate mitotic exit, interacts with Tem1p and Lte1p; localizes to regions of polarized growth; potential Cdc28p substrate	S503; S613; S691; Y700; S704; S742; S748; T755; T1001; S1003	S67	CLB2, CDC28			7, 32, 116, 122, 142, 373, 374, 379
			S503	CDC28			7, 116, 142, 373, 379
			S613	CDC28	CDC28		7, 37, 116, 122, 139, 142, 217,

						370, 373, 374, 379
			S689	CDC28		7, 116, 142, 217, 370, 373, 374, 379
NVJ1	Nuclear envelope protein; anchored to the nuclear inner membrane, that interacts with the vacuolar membrane protein Vac8p to promote formation of nucleus-vacuole junctions during piecemeal microautophagy of the nucleus (PMN)	S156; S182; T187; S188; S190; S199; T251; S285; S290	S250	SNF1		32, 139, 370, 379
			S298	CDC28		7, 116, 142, 217, 373, 379
			T251	SNF1		7, 32, 370, 379
RTS1	B-type regulatory subunit of protein phosphatase 2A (PP2A); Rts1p and Cdc55p are alternative regulatory subunits for PP2A catalytic subunits, Pph21p and Pph22p; PP2A-Rts1p protects cohesin when recruited by Sgo1p to the pericentromere; highly enriched at centromeres in the absence of Cdc55p; required for maintenance of septin ring organization during cytokinesis, for ring disassembly in G1 and for dephosphorylation of septin, Shs1p; homolog of the mammalian B' subunit of PP2A		S263	YPL150W		32, 152
			T242	CDC28		7, 139, 142, 217, 379
FPR3	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; affects expression of multiple genes via its role in nucleosome assembly; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; PPIase domain acts as a transcriptional repressor when tethered to		S80	KSP1	CMP2	7, 32, 37, 116, 142, 152, 217, 373, 433

	DNA by lexA, and repressor activity is dependent on PPIase activity; FPR3 has a paralog, FPR4, that arose from the whole genome duplication					
			S81	KSP1	CMP2	7, 32, 37, 116, 142, 152, 217, 373
			S186	CKA1, CKA2		426
			T89	SSK2		32, 142
			Y184	CKA1, CKA2, CKB1, CKB2	MSG5	243, 425, 426
SEC31	Component of the Sec13p-Sec31p complex of the COPII vesicle coat; COPII coat is required for vesicle formation in ER to Golgi transport; mutant has increased aneuploidy tolerance	T996; S997; S999	S836	CDC28		7, 116, 122, 142, 373, 379
			S974	RAD53		7, 100, 142, 370, 374, 379
			S980	CDC28		7, 32, 100, 142, 374, 379
			S988	KIN82		32, 142, 379
			S992	KIN82		7, 32, 100, 139, 142, 217, 374, 379
HAL5	Putative protein kinase; overexpression increases sodium and lithium tolerance, whereas gene disruption increases cation and low pH sensitivity and impairs potassium uptake, suggesting a role in regulation of Trk1p and/or Trk2p transporters; HAL5 has a paralog, KKQ8, that arose from the whole genome duplication		S64	CDC28		142, 152
			S229	MCK1		32

			S233	MCK1		7, 32, 142, 374, 379
TEM1	GTP-binding protein of the Ras superfamily; involved in termination of M-phase; controls actomyosin and septin dynamics during cytokinesis	S236; S240	S240		CDC28	139, 142, 152, 379
UME6	Rpd3L histone deacetylase complex subunit; key transcriptional regulator of early meiotic genes; involved in chromatin remodeling and transcriptional repression via DNA looping; binds URS1 upstream regulatory sequence, represses transcription by recruiting conserved histone deacetylase Rpd3p (through co-repressor Sin3p) and chromatin-remodeling factor Isw2p; couples metabolic responses to nutritional cues with initiation and progression of meiosis, forms compl	S316; S318; S321; T403	S107	MCK1, MRK1, RIM11		32, 142, 379, 436
			S316	FRK1		7, 32, 142, 152, 217, 379
			T99	MCK1, MRK1, RIM11		32, 142, 244, 379, 436
			T103	MCK1, MRK1, RIM11		32, 379, 436
AKR1	Palmitoyl transferase involved in protein palmitoylation; acts as a negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; contains ankyrin repeats; AKR1 has a paralog, AKR2, that arose from the whole genome duplication; any of several human homologs encoding DHHC-type zinc fingers (ZDHHC) can complement temperature sensitivity of yeast akr1 null mutant	S51; S57	S57	TPK3	CKA1	7, 32, 116, 139, 142, 152, 217, 370, 373, 379
CAT8	Zinc cluster transcriptional activator; necessary for derepression of a variety of	S173	S562	SNF1		48

	genes under non-fermentative growth conditions, active after diauxic shift, binds carbon source responsive elements; relative distribution to the nucleus increases upon DNA replication stress				
YMR124W; EPO1	Protein involved in septin-ER tethering; interacts with ER membrane protein, Scs2p, and Shs1p, a septin ring component, at bud neck to create ER diffusion barrier; GFP-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; interacts with Crm1p in two-hybrid assay; YMR124W has a paralog, YLR031W, that arose from the whole genome duplication	Y355; S356	S586	CLB2, CDC28	142, 379
NUP60	FG-nucleoporin component of central core of the nuclear pore complex; contributes directly to nucleocytoplasmic transport and maintenance of the nuclear pore complex (NPC) permeability barrier and is involved in gene tethering at the nuclear periphery; relocalizes to the cytosol in response to hypoxia; both NUP1 and NUP60 are homologous to human NUP153	S70; S78; S81; S312	S162	PTK1	7, 32, 116, 142, 373, 379
			S222	CLB2, CDC28	142, 379
			S312	CDC28	7, 142, 370, 379
			S360	RAD53	7, 56, 370, 379
			S382	CDC28, RAD53	7, 32, 56, 122, 142, 370, 374, 379
			S480	RAD53	7, 52, 56, 116, 370, 373, 379
			S483	RAD53	7, 52, 56, 370, 379

			T460	CDC28		7, 32, 116, 142, 373, 379
TIF4631	Translation initiation factor eIF4G; subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); interacts with Pab1p and with eIF4A (Tif1p); also has a role in biogenesis of the large ribosomal subunit; TIF4631 has a paralog, TIF4632, that arose from the whole genome duplication	S163; S191; S194; S195; S232; T241; T242; T276	S522	KSP1	SIW14	32, 152, 379
TIF4632	Translation initiation factor eIF4G; subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); TIF4632 has a paralog, TIF4631, that arose from the whole genome duplication		T196	CDC28		7, 116, 139, 142, 370, 373, 374, 379
			T301	CDC28		142, 217
RPH1	JmjC domain-containing histone demethylase; targets tri- and dimethylated H3K36; associates with actively transcribed regions and promotes elongation; repressor of autophagy-related genes in nutrient-replete conditions; damage-responsive repressor of PHR1; phosphorylated by the Rad53p-dependent DNA damage checkpoint pathway and by a Rim1p-mediated event during starvation; target of stress-induced hormesis; RPH1 has a paralog, GIS1, that arose from the whole genome duplication	S459; S557; S561; S688; S689	S139	RAD53		52
			S430	CDC28		7, 32, 139, 142, 152, 379
			S561	CDC28		7, 32, 116, 142, 152, 217, 373, 379
			S575	CDC28		7, 142, 379

BEM2	Rho GTPase activating protein (RhoGAP); involved in the control of cytoskeleton organization and cellular morphogenesis; required for bud emergence; potential GAP for Rho4p		T1038	CDC28		142, 379
BOI2	Protein implicated in polar growth, functionally redundant with Boi1p; interacts with bud-emergence protein Bem1p; contains an SH3 (src homology 3) domain and a PH (pleckstrin homology) domain; BOI2 has a paralog, BOI1, that arose from the whole genome duplication	T372; S373; S375; S666; S667	S450	CDC28		32, 142, 217
			S457	CDC28		32, 142, 217
			S519	CDC28	CDC28	7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 374, 379
			S523	CDC28	CDC28	7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 374, 379
			S652	CLB2, CDC28		122, 142, 217, 374, 379
GTT3	Protein of unknown function may be involved in glutathione metabolism; function suggested by computational analysis of large-scale protein-protein interaction data; N- and C-terminal fusion proteins localize to the cell periphery	S116; T120; S121; T123	S116	CTK1		32, 142, 217, 370, 374, 379
ZRG8	Protein of unknown function; authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; GFP-fusion protein is localized to the cytoplasm; transcription induced under conditions of zinc deficiency	S676	S365			32, 56

			S914				142, 379
GIP2	Putative regulatory subunit of protein phosphatase Glc7p; involved in glycogen metabolism; contains a conserved motif (GVNK motif) that is also found in Gac1p, Pig1p, and Pig2p; GIP2 has a paralog, PIG2, that arose from the whole genome duplication		S213	CDC28			142
YER079W	Putative protein of unknown function	T31; S39; S41; Y186; S189; S192; S194; S197; T201	S39		RIM11	SIT4	7, 32, 139, 142, 374
			S41	CDC28		SIT4	7, 32, 142, 374, 379
			S189	TPK3			7, 32, 142, 370, 379
			S192	TPK3			7, 32, 142, 370, 379
			S194	CKA1			7, 32, 142, 379
			T53			SIT4	32
SCS2	Integral ER membrane protein, regulates phospholipid metabolism; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to plasma membrane (PM) and regulate PI4P levels by controlling access of Sac1p phosphatase to substrate PI4P in the PM; interacts with FFAT motifs in Opi1p, Swh1p, Osh2p, and Osh3p; involved in telomeric silencing; VAP homolog; SCS2 has a paralog, SCS22, that arose from the whole genome duplication	T204	T204	CLB2, CDC28			32, 139, 142, 379
SOK1	Protein of unknown function; overexpression suppresses the growth defect of mutants lacking protein kinase A activity; involved in cAMP-mediated signaling; localized to the nucleus; similar to the mouse testis-specific protein PBS13	S193; S197	S191	CDC28			7, 116, 142, 373, 374, 379

			S193	CDC28			7, 116, 142, 373, 374, 379
YTA7	Protein that localizes to chromatin; has a role in regulation of histone gene expression; has a bromodomain-like region that interacts with the N-terminal tail of histone H3, and an ATPase domain; relocalizes to the cytosol in response to hypoxia; potentially phosphorylated by Cdc28p	S11; S1142	S1142	MEC1, TEL1	CKA2		7, 32, 37, 52, 116, 139, 142, 369, 370, 373, 374, 379
PFK26	6-phosphofructo-2-kinase; inhibited by phosphoenolpyruvate and sn-glycerol 3-phosphate; has negligible fructose-2,6-bisphosphatase activity; transcriptional regulation involves protein kinase A	S42; S43; S667; S671; S673; S674; S675	S652	TPK1			7, 139, 142, 217, 370, 379
			T157	TPK1			7, 56, 82, 142, 217, 370, 379
VHS2	Regulator of septin dynamics; involved in the regulation of septin dynamics at bud neck after mitotic entry, likely by stabilizing septin structure; regulated at post-translational level by cell cycle dependent phosphorylation; likely phosphorylated by Cdc28p and dephosphorylated by Cdc14p before cytokinesis; high-copy suppressor of synthetic lethality of sis2 sit4 double mutant; VHS2 has a paralog, MLF3, that arose from the whole genome duplication		S202			SIT4	32
			S301	CDC28	CDC28		7, 139, 142, 152, 217, 374, 379
			S325			PTP1	32, 142, 152, 217
			S330			PTP1	32, 142, 152
ASG1	Zinc cluster protein proposed to be a transcriptional regulator; regulator involved in the stress response; null mutants have a respiratory deficiency, calcofluor white		S166	MEC1, TEL1			7, 52, 370

	sensitivity and slightly increased cycloheximide resistance				
NUP159	FG-nucleoporin component of central core of the nuclear pore complex; also part of the nuclear pore complex (NPC) cytoplasmic filaments; contributes directly to nucleocytoplasmic transport; regulates ADP release from the ATP-dependent RNA helicase Dbp5p; forms a stable association with Nup82p, Gle2p and two other FG-nucleoporins (Nsp1p and Nup116p)	S402; S404; S940; T948	S182	DUN1	52, 142
			S735	CDC28	7, 116, 122, 142, 217, 373, 379
			S854	CLB2, CDC28	142
HOS4	Subunit of the Set3 complex; complex is a meiotic-specific repressor of sporulation specific genes that contains deacetylase activity; potential Cdc28p substrate		S38	SNF1	32, 142, 370, 379
			S290	CLB2, CDC28	142, 379
			S690	CDC28	7, 32, 122, 142, 152, 217, 370, 374, 379
			T37	SNF1	32, 142
MOB1	Component of the mitotic exit network; associates with and is required for the activation and Cdc15p-dependent phosphorylation of the Dbf2p kinase; required for cytokinesis and cell separation; component of the CCR4 transcriptional complex; relocalizes from cytoplasm to the nuclear periphery upon DNA replication stress		S36	CDC28	7, 32, 37, 116, 122, 142, 152, 217, 373, 374, 379
			S80	CLB2, CDC28	7, 32, 37, 100, 139, 142, 217,

					370, 374, 379
SLM1	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; TORC2 complex substrate and effector; protein abundance increases in response to DNA replication stress; SLM1 has a paralog, SLM2, that arose from the whole genome duplication	S145; S150	S157	PKH3	32, 370
			S158	PKH3	32, 370
			S659	PKH1, PKH2	67
YRB2	Protein of unknown function; involved in nuclear processes of the Ran-GTPase cycle; involved in nuclear protein export; contains Ran Binding Domain and FxFG repeats; interacts with Srm1p, GTP-Gsp1p, Rna1p and Crm1p; relocalizes to the cytosol in response to hypoxia; not essential for viability	T117; T123; T124; S125; T126; S128	S14		7, 116, 142, 370, 373
			T31		7, 32, 139, 142, 370, 374, 379
ULP2	Peptidase that deconjugates Smt3/SUMO-1 peptides from proteins; plays a role in chromosome cohesion at centromeric regions and recovery from checkpoint arrest induced by DNA damage or DNA replication defects; potential Cdc28p substrate; human homolog PML implicated in promyelocytic leukemia can partially complement yeast null mutant		S788	CDC28	7, 142, 379
			S795	CDC28	142, 379
			S984	CLB2, CDC28	142, 374, 379
AIM21	Protein of unknown function; involved in mitochondrial migration along actin filament; may interact with ribosomes; GFP-	S36; T40; T84; S119; T121; T180; S183; S185; S281;	S183	PSK2	7, 32, 116, 142, 152, 217, 370,

	fusion protein colocalizes with Sac1p to the actin cytoskeleton	T282; S476; S477; T480; T552			373, 374, 379
			T180	PSK2	7, 32, 142, 152, 217, 370, 374, 379
BUD6	Actin- and formin-interacting protein; participates in actin cable assembly and organization as a nucleation-promoting factor (NPF) for formins Bni1p and Bnr1p; a triple helical coiled-coil domain in the C-terminal region interacts with Bni1p; involved in polarized cell growth; isolated as bipolar budding mutant; potential Cdc28p substrate	S233	S327	CDC28	7, 12, 32, 116, 142, 217, 370, 373, 374, 379
MAF1	Highly conserved negative regulator of RNA polymerase III; involved in tRNA processing and stability; inhibits tRNA degradation via rapid tRNA decay (RTD) pathway; binds N-terminal domain of Rpc160p subunit of Pol III to prevent closed-complex formation; regulated by phosphorylation mediated by TORC1, protein kinase A, Sch9p, casein kinase 2; localizes to cytoplasm during vegetative growth and translocates to nucleus and nucleolus under stress conditions		S90	TPK1	7, 32, 142, 203, 217, 267, 374, 379
			S101	TPK1	203, 267, 379
			S159	CKA1, CKA2, CKB1, CKB2	119, 379
			S160	CKA1, CKA2, CKB1, CKB2	119
			S161	CKA1, CKA2,	119

				CKB1, CKB2	
			S162	CKA1, CKA2, CKB1, CKB2	119
			S177	TPK1	32, 56, 142, 152, 203, 267
			S178	TPK1	32, 142, 152, 203, 267, 379
			S179	SCH9	32, 139, 152, 379
			S209	TPK1	142, 203, 217, 267, 374
			S210	TPK1	7, 203, 217, 267
			S388	CKA1, CKA2, CKB1, CKB2	119
VNX1	Calcium/H+ antiporter localized to the endoplasmic reticulum membrane; member of the calcium exchanger (CAX) family; potential Cdc28p substrate	S110; T118; S120; S121	S121	CLB2, CDC28	7, 116, 142, 152, 189, 217, 373, 379
			T118	CLB2, CDC28	142
YFL042C; LAM5	Putative sterol transfer protein; one of six StART-like domain-containing proteins in yeast that may be involved in sterol transfer between intracellular membranes; conserved across eukaryotes; has both GRAM and StART-like (VASt) domains; localizes to membrane contact sites throughout the cell, including nucleus-vacuole junctions and ER-mitochondrial contact sites	T110	S103	CDC28	142, 374, 379
			S149	CDC28	139, 142, 217, 379

			T110	CDC28	7, 142, 152, 217, 379
GAT1	Transcriptional activator of nitrogen catabolite repression genes; contains a GATA-1-type zinc finger DNA-binding motif; activity and localization regulated by nitrogen limitation and Ure2p; different translational starts produce two major and two minor isoforms that are differentially regulated and localized	T369; S373	S360	PTK1	32, 456
BLM10	Proteasome activator; binds the core proteasome (CP) and stimulates proteasome-mediated protein degradation by inducing gate opening; required for sequestering CP into proteasome storage granule (PSG) during quiescent phase and for nuclear import of CP in proliferating cells; required for resistance to bleomycin, may be involved in protecting against oxidative damage; similar to mammalian PA200	S11; S29; S34; S35; S36; S62; T64	S11	CDC28	7, 116, 142, 181, 373
			S29	CLB2, CDC28	7, 32, 56, 116, 142, 181, 373, 374, 379
			S56	BUD32	7, 32, 56, 100, 139, 142, 152, 181, 217, 370, 374, 379
YPI1	Regulatory subunit of the type I protein phosphatase (PP1) Glc7p; Glc7p participates in the regulation of a variety of metabolic processes including mitosis and glycogen metabolism; in vitro evidence suggests Ypi1p is an inhibitor of Glc7p while in vivo evidence suggests it is an activator; overproduction causes decreased cellular content of glycogen; partial depletion causes	S133	S131	PSK1	7, 32, 37, 56, 116, 139, 142, 217, 370, 373, 374

	lithium sensitivity, while overproduction confers lithium-tolerance				
			S133	PSK1	7, 32, 37, 56, 116, 122, 142, 217, 370, 373, 374, 379
IGD1	Cytoplasmic protein that inhibits Gdb1p glycogen debranching activity; required for normal intracellular accumulation of glycogen; phosphorylated in vivo; expression increases during wine fermentation; protein abundance increases in response to DNA replication stress; IGD1 has a paralog, YOL024W, that arose from the whole genome duplication	S14	S95	TPK3	7, 32, 100, 142, 370
LSB3	Protein containing a C-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization; protein abundance increases in response to DNA replication stress; LSB3 has a paralog, YSC84, that arose from the whole genome duplication	T298; S300; S303; S311; S397; S399; T400; S401; S402	S255	CKA1	32
			S256	CKA1	32
CKB1	Beta regulatory subunit of casein kinase 2 (CK2); a Ser/Thr protein kinase with roles in cell growth and proliferation; CK2, comprised of CKA1, CKA2, CKB1 and CKB2, has many substrates including transcription factors and all RNA polymerases	S111	S111	RIO1	7, 32, 152, 370
SUM1	Transcriptional repressor that regulates middle-sporulation genes; required for mitotic repression of middle sporulation-specific genes; also acts as general replication initiation factor; involved in telomere maintenance, chromatin silencing; regulated by pachytene checkpoint	S378	S379	CDC28	7, 142, 152, 228, 370, 379

			S712	MEC1, TEL1			7, 52, 142, 370, 379, 527
			S738	CLB2, CDC28			7, 142, 228, 374, 379
			T306	IME2			3, 271
CTK3	Gamma subunit of C-terminal domain kinase I; CTDK-I phosphorylates RNA polymerase II subunit Rpo21p to affect transcription and pre-mRNA 3' end processing, and also phosphorylates ribosomal protein Rps2p to increase translational fidelity; protein abundance increases in response to DNA replication stress	T34; T35	T34	CTK1			32, 100, 370, 374
MTC1	Protein of unknown function that may interact with ribosomes; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to COPI-coated vesicles (early Golgi); mtc1 is synthetically lethal with cdc13-1	T330; S336; S337; S339; S340; S342	S273		CKA2	YCH1	7, 32, 139, 142, 217, 379
ALY2	Alpha arrestin; controls nutrient-mediated intracellular sorting of permease Gap1p; interacts with AP-1 subunit Apl4p; phosphorylated by Npr1p and also by cyclin-CDK complex Pcl7p-Pho85p; promotes endocytosis of plasma membrane proteins; ALY2 has a paralog, ALY1, that arose from the whole genome duplication	S155; S168; S172; S213; S740; S741	S176	CLB2, CDC28			142
			S213	CDC28			7, 32, 122, 142, 152, 374, 379
NET1	Core subunit of the RENT complex; involved in nucleolar silencing and telophase exit; stimulates transcription by RNA polymerase I and regulates nucleolar structure; NET1 has a paralog, TOF2, that arose from the whole genome duplication	S231	S30	CDC5			363
			S31	CDC5			363

	S48	CDC5		236, 363, 379
	S56	CDC5		236
	S60	CDC5		37, 142, 152, 236, 363, 379
	S64	CDC5		152, 236, 363, 379
	S166	CDC28		20, 32, 116, 142, 152, 373, 379
	S169	CDC28		32
	S223	CDC5		363
	S224	CDC5		363
	S228	CDC5	CKA2	7, 37, 139, 142, 152, 236, 363, 374, 379
	S231	CDC5		7, 20, 37, 142, 152, 217, 236, 363, 374, 379
	S242	CDC5		152, 236, 363, 379
	S252	CDC28		7, 20, 32, 37, 122, 142, 152, 236, 379
	S259	CDC5		20, 32, 152, 236, 379
	S269	CDC5		152, 236, 379
	S280	CDC5		236
	S295	CDC5	SNF1	139, 142, 152, 363, 379
	S301	CDC5		363
	S335	CDC5		363

			S447	CLB2, CDC28		32, 37, 142, 379
			S452	CLB2, CDC28		32, 142
			S830	CDC28		7, 32, 37, 142
			S840	RAD53		7, 37, 56, 370, 379
			S1032	CLB2, CDC28	CDC28	7, 20, 32, 116, 139, 142, 217, 373, 374, 379
			S1056	CLB2, CDC28		32, 37, 142, 152, 379
			T16	CDC5		363
			T192	CDC5		236
			T194	CDC5		363
			T195	CDC5		363
			T196	CDC5		363
			T197	CDC5		363
			T288	CDC5		236
			T297	CDC28		142, 152, 363, 379
			T302	CDC5		363
			T676	CLB2, CDC28		20, 32, 56, 142, 152, 217, 374, 379
			T1042	CLB2, CDC28		7, 32, 37, 142, 152, 370, 379
BBC1	Protein possibly involved in assembly of actin patches; interacts with an actin assembly factor Las17p and with the SH3 domains of Type I myosins Myo3p and Myo5p; localized predominantly to cortical actin patches	S77; S78; T81; S83; S103; S158; S620; S621; T624; T810; S815; T818; T820; S822; T824; T835; T894; T895; S902	S103	CDC28	PHO85	7, 32, 56, 116, 139, 142, 217, 370, 373, 374, 379

			S631	MKK1		7, 32, 122, 142, 152, 217, 379
			S634	MKK1		7, 32, 142, 152, 217, 379
			S638	MKK1		32, 116, 122, 142, 152, 217, 373, 379
			T636	MKK1		32, 116, 122, 142, 152, 373, 379
PTK2	Serine/threonine protein kinase; involved in regulation of ion transport across plasma membrane; carboxyl terminus is essential for glucose-dependent Pma1p activation via phosphorylation of Pma1p-Ser899; enhances spermine uptake; PTK2 has a paralog, PTK1, that arose from the whole genome duplication	T56; S57; S59; S61; S63; S65; S69; S73; S585; T586; S587; T588; S592; S595; S711; S726; T727; T729; T730; T732; S773; S775; S776	S69	CLB2, CDC28		37, 142, 152, 379
			S711	PTK2	CKA2	7, 32, 37, 139, 142, 217, 374, 379
			S752	PTK2		7, 32, 116, 142, 217, 373, 374, 379
			S755	PTK2		32, 142, 217, 379
			S784	CLB2, CDC28		7, 32, 37, 142, 379
			T727	CDC28		142, 217
			T730	CDC28		7, 37, 116, 142, 217, 373, 379

			T737	CDC28	116, 142, 217, 373, 379
ENT3	Protein containing an N-terminal epsin-like domain; involved in clathrin recruitment and traffic between the Golgi and endosomes; associates with the clathrin adaptor Gga2p	S148	S203	BUD32	7, 32, 142, 152, 217, 379
ASK10	Regulator of the Fps1p glycerol channel; under nonstress conditions, binds to Fps1p to positively regulate glycerol transport; under osmotic stress, multiple phosphorylation by Hog1p causes Ask10p to dissociate from Fps1p; forms homodimers and heterodimerizes with paralog Rgc1p; phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p; associates with RNA polymerase II holoenzyme	S1070	T808	CDC28	7, 32, 37, 142, 152, 379
SEC16	COPII vesicle coat protein required for ER transport vesicle budding; essential factor in endoplasmic reticulum exit site (ERES) formation, as well as in COPII-mediated ER-to-Golgi traffic; bound to periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p	S28; S30; T2127; S2128; S2130; T2132	S607	CDC28	7, 116, 122, 142, 370, 373, 379
			S841	CTK1	32, 152, 217, 379
			S1515	CDC28	7, 32, 122, 142, 152, 217, 374, 379
LYS20	Homocitrate synthase isozyme and functions in DNA repair; catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; LYS20 has a paralog, LYS21, that arose from the whole genome duplication	T396	T396	CDC28	7, 32, 56, 116, 122, 142, 152, 217, 370, 373, 374, 379

YGR237C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	S125; S127	S117		32, 142, 152, 379
TAF4	TFIID subunit (48 kDa); involved in RNA polymerase II transcription initiation; potential Cdc28p substrate	S4; S9; S80	S36	CLB2, CDC28	7, 32, 56, 116, 142, 217, 373
			S49	CDC28	7, 32, 116, 142, 373, 379
PSP2	Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of group II intron-splicing defects of a mutation in MRS2 and of a conditional mutation in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing		S340	CDC28	7, 32, 139, 142, 217, 374, 379
INP52	Polyphosphatidylinositol phosphatase; dephosphorylates a number of phosphatidylinositol phosphates (PtdInsPs, PIPs) to PI; involved in endocytosis; hyperosmotic stress causes translocation to actin patches; synaptojanin-like protein with a Sac1 domain; INP52 has a paralog, INP53, that arose from the whole genome duplication	S1081; S1082	S1005	CLB2, CDC28	32, 116, 122, 142, 152, 217, 373, 379
			S1016	CLB2, CDC28	32, 142, 152, 217, 379
SKP1	Evolutionarily conserved kinetochore protein; part of multiple protein complexes, including the SCF ubiquitin ligase complex, the CBF3 complex that binds centromeric DNA, and the RAVE complex that regulates assembly of the V-ATPase; protein abundance increases in response to DNA replication stress	S45; S49	S45	PHO85	32, 142, 152, 379
			S47	PHO85	32, 379
			S49	PTK1	32, 142, 152, 379
			T3	MPS1	37

MDS3	Putative component of the TOR regulatory pathway; negative regulator of early meiotic gene expression; required, with Pmd1p, for growth under alkaline conditions; has an N-terminal kelch-like domain; MDS3 has a paralog, PMD1, that arose from the whole genome duplication	S668; S669; S671; S693; S781; S918; S919; T920; T923; T1156; S1166; T1168	S693	CDC28		7, 32, 37, 116, 142, 217, 370, 373, 374, 379
			S1387	CLB2, CDC28		142, 379
SDS23	Protein involved in cell separation during budding; one of two S. cerevisiae homologs (Sds23p and Sds24p) of the S. pombe Sds23 protein, which is implicated in APC/cyclosome regulation; SDS23 has a paralog, SDS24, that arose from the whole genome duplication	S61; T66; S398; S399; S400; S402; S404; T405; T409; T410; S430	T405	CDC28		142, 217, 379
YGR054W	Eukaryotic initiation factor eIF2A; associates specifically with both 40S subunits and 80 S ribosomes, and interacts genetically with both eIF5b and eIF4E; homologous to mammalian eIF2A	S473; S560; S561; T563; S564; S567; T568; S572; T581; T586; S587	S560	MCK1	TPK1	7, 32, 139, 142, 370, 374
			S561	MCK1		7, 32, 142, 370, 374
			S564	MCK1		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			T563	MCK1		7, 32, 116, 142, 152, 217, 370, 373, 374
			T568	MCK1		7, 32, 142, 379
DAM1	Essential subunit of the Dam1 complex (aka DASH complex); cooperates with Duo1p to connect the DASH complex with the microtubules (MT); couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation;		S20	IPL1		49, 139, 142, 177, 254, 374, 379, 392

	Ipl1p target for regulating kinetochore-MT attachments					
			S257	IPL1		49, 142, 177, 254, 374, 379
			S265	IPL1		49, 142, 177, 254, 379
			S292	IPL1		49, 142, 177, 374, 379
YGR130C	Component of the eisosome with unknown function; GFP-fusion protein localizes to the cytoplasm; specifically phosphorylated in vitro by mammalian diphosphoinositol pentakisphosphate (IP7)	S44; S249; T254; S257; T277; T278; S281; S284; S286; T337; S338; T339; T342	S343	TPK3		32, 217, 370, 379
			S347	YPK1		32, 217, 370, 379
PBP1	Component of glucose deprivation induced stress granules; involved in P-body-dependent granule assembly; similar to human ataxin-2; interacts with Pab1p to regulate mRNA polyadenylation; interacts with Mkt1p to regulate HO translation; protein increases in abundance and relative distribution to the nucleus increases upon DNA replication stress		S436	CLB2, CDC28		7, 32, 142, 217, 278, 373, 374
DCP2	Catalytic subunit of Dcp1p-Dcp2p decapping enzyme complex; removes 5' cap structure from mRNAs prior to their degradation; also enters nucleus and positively regulates transcription initiation; nudix hydrolase family member; forms cytoplasmic foci upon DNA replication stress; human homolog DCP2 complements yeast dcp2 thermosensitive mutant	S598; S747; S751	S137	STE20		446
HHO1	Histone H1, linker histone with roles in meiosis and sporulation; decreasing levels early in sporulation may promote meiosis, and increasing levels during sporulation	S130; S173; S174; S176; S177	S130		SIW14	32, 116, 373

	facilitate compaction of spore chromatin; binds to promoters and within genes in mature spores; may be recruited by Ume6p to promoter regions, contributing to transcriptional repression outside of meiosis; suppresses DNA repair involving homologous recombination				
FPK1	Ser/Thr protein kinase; phosphorylates several aminophospholipid translocase family members, regulating phospholipid translocation and membrane asymmetry; phosphorylates and inhibits upstream inhibitory kinase, Ypk1p; localizes to the cytoplasm, early endosome/TGN compartments and thplasma membrane; localizes to the shmoo tip where it has a redundant role in the cellular response to mating pheromone; FPK1 has a paralog, KIN82, that arose from the whole genome duplication	S200; S462; T674; S676	S137	CDC28	142, 379
			S140	CDC28	7, 32, 142, 152, 379
			S144	CDC28	32, 142, 152, 379
			S175	CDC28	7, 142
			S198	CDC28	142
			S339	CDC28	7, 142, 152, 370, 379
			T201	CDC28	142
MDG1	Plasma membrane protein; involved in G-protein mediated pheromone signaling pathway; overproduction suppresses bem1 mutations; MDG1 has a paralog, CRP1, that arose from the whole genome duplication	S160; T164; S178; T180; T181; T182; S227; T256; S257; S263; S272	S288	CKA1	7, 32, 116, 122, 142, 152, 373, 374, 379
			S291	PSK2	7, 32, 116, 122, 142, 373, 374, 379
			T290	PSK2	7, 32, 116, 122, 142,

					152, 373, 374
BNI5	Linker protein responsible for recruitment of myosin to the bud neck; interacts with the C-terminal extensions of septins Cdc11p and Shs1p and binds Myo1p to promote cytokinesis	S263; S270; S273; T274; T280	S270	SNF1	7, 32, 100, 139, 142, 217, 280, 370, 374, 379
			S273		7, 32, 100, 142, 217, 280, 281, 370, 379
			T274		7, 32, 100, 142, 280, 370, 379
CBK1	Serine/threonine protein kinase of the the RAM signaling network; Ndr/LATS family member; binds regulatory subunit Mob2p; involved in regulation of cellular morphogenesis, polarized growth, and septum destruction; phosphorylation by Cbk1p regulates localization and activity of Ace2p transcription factor and Ssd1p translational repressor; Cbk1p activity is regulated by both phosphorylation and specific localization; relocalizes to cytoplasm upon DNA replication stress	S63; S66	S570	CBK1	155, 300
			T93	CLB2, CDC28	142
			T109	CLB2, CDC28	7, 142, 379
IGO1	Protein required for initiation of G0 program; prevents degradation of nutrient-regulated mRNAs via the 5'-3' mRNA decay pathway; phosphorylated by Rim15p; GFP protein localizes to the cytoplasm and nucleus; IGO1 has a paralog, IGO2, that arose from the whole genome duplication	S7	S64	RIM15	7, 32, 116, 139, 142, 166, 217, 344, 362, 373, 374, 379, 385, 386
NSG2	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that	S49; S81; S82	S90	YPK1	7, 32, 100, 142, 152,

	catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; NSG2 has a paralog, NSG1, that arose from the whole genome duplication				217, 370, 374, 379
			S92	YPK1	32, 142, 217, 370, 379
			S93	YPK1	7, 32, 100, 142, 152, 217, 370, 374, 379
CRZ1	Transcription factor, activates transcription of stress response genes; nuclear localization is positively regulated by calcineurin-mediated dephosphorylation; rapidly localizes to the nucleus under blue light stress; can be activated in stochastic pulses of nuclear localization in response to calcium		S409	TPK1	170
			S410	TPK1	142, 170, 370, 379
			S423	TPK1	32, 56, 170
			S427	TPK1	7, 32, 56, 170, 379
			S429	TPK1	7, 32, 170, 379
SUR7	Plasma membrane protein, component of eisosomes; long-lived protein that remains stable in eisosomes of mother cells while other eisosome proteins, Pil1p and Lsp1p, turn over; may function to anchor the eisosome in place; sporulation and plasma membrane sphingolipid content are altered in mutants; localizes to furrow-like invaginations (MCC patches)	T249; T251; S259; S261; S266; S267; T273; S293; S301	S261	TPK3	32, 379
GPD1	NAD-dependent glycerol-3-phosphate dehydrogenase; key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high-osmolarity glycerol response pathway;	S23; S24; S25; S27	S24	CTK1	7, 32, 100, 116, 122, 142, 152, 168, 217,

	protein abundance increases in response to DNA replication stress; constitutively inactivated via phosphorylation by the protein kinases Ypk1p and Ypk2p, dephosphorylation increases catalytic activity; forms a heterodimer with Pnc1p to facilitate its peroxisomal import			294, 370, 373, 379
		S27	CTK1	7, 32, 100, 116, 122, 142, 152, 168, 217, 294, 370, 373, 374, 379
CDC14	Protein phosphatase required for mitotic exit; required for rDNA segregation, cytokinesis, meiosis I spindle disassembly, environmental stress response; held in nucleolus by Cdc55p in early meiosis, liberated by FEAR and Mitotic Exit Network in anaphase, enabling it to effect a decrease in CDK/B-cyclin activity and mitotic exit; sequestered in metaphase II, released upon entry into anaphase II; human homolog CDC14A can complement thermosensitivity of yeast cdc14-1 mutant	S429	CDC28	32, 142, 152, 165, 219, 370, 379
		S531	DBF2, MOB2	266
		S537	DBF2, MOB2	165, 266, 379
		S546	DBF2, MOB2	165, 266, 379
		S548	DBF2, MOB2	266
SLT2	Serine/threonine MAP kinase; coordinates expression of all 19S regulatory particle assembly-chaperones (RACs) to control proteasome abundance; involved in regulating maintenance of cell wall integrity, cell cycle progression, nuclear mRNA	S423	RAD53	7, 37, 379, 398

	retention in heat shock, septum assembly; required for mitophagy, pexophagy; affects recruitment of mitochondria to phagophore assembly site; plays role in adaptive response of cells to cold; regulated by the PKC1-mediated signaling pathway					
			S428	MEC1, TEL1		7, 37, 398
REG1	Regulatory subunit of type 1 protein phosphatase Glc7p; involved in negative regulation of glucose-repressible genes; involved in regulation of the nucleocytoplasmic shuttling of Hxk2p; REG1 has a paralog, REG2, that arose from the whole genome duplication	S254; Y497; S570; S572; S576; T579; S582; S775; T776; S778; Y780; S976; S977; S1013; S1014	S421	CDC28		7, 32, 37, 142, 217, 370, 379
			S898	CDC28		7, 142, 379
			T896	CDC28		142, 379
BCK1	MAPKKK acting in the protein kinase C signaling pathway; the kinase C signaling pathway controls cell integrity; upon activation by Pkc1p phosphorylates downstream kinases Mkk1p and Mkk2p; MAPKKK is an acronym for mitogen-activated protein (MAP) kinase kinase kinase	S250	S411			7, 37, 142, 379
			S747			7, 142, 217, 379
			S816			37, 56, 142, 379
RSC4	Component of the RSC chromatin remodeling complex; found in close proximity to nucleosomal DNA; displaced from the surface of nucleosomal DNA after chromatin remodeling; acetylated (K25) by Gcn5p, altering replication stress tolerance; contains tandem bromodomains that recognize histone H3 acetylated on K14 (H3K14ac) by Gcn5p		S545	MEC1, TEL1		7, 52, 379
RPL6A	Ribosomal 60S subunit protein L6A; N-terminally acetylated; binds 5.8S rRNA;		S12		SIT4	7, 32, 122, 139, 142,

	homologous to mammalian ribosomal protein L6, no bacterial homolog; RPL6A has a paralog, RPL6B, that arose from the whole genome duplication					370, 374, 379
MLP1	Myosin-like protein associated with the nuclear envelope; nuclear basket protein that connects the nuclear pore complex with the nuclear interior; involved with Tel1p in telomere length control; involved with Pml1p and Pml39p in nuclear retention of unspliced mRNAs; MLP1 has a paralog, MLP2, that arose from the whole genome duplication	S333; T337	S1670	DUN1		7, 32, 52
			S1675	CDC28		7, 32, 370, 379
			S1710	RAD53		7, 139, 142, 370, 379
			S1723	DUN1		7, 52
VTC3	Regulatory subunit of the vacuolar transporter chaperone (VTC) complex; involved in membrane trafficking, vacuolar polyphosphate accumulation, microautophagy and non-autophagic vacuolar fusion; VTC3 has a paralog, VTC2, that arose from the whole genome duplication	S270; S274; S621; S622	S274		SIT4	7, 32, 116, 142, 152, 373, 379
			S621	CTK1	PPQ1	7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			S622	CTK1	PPQ1	7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			T627	CTK1		7, 32, 116, 142, 373
ROD1	Alpha-arrestin involved in ubiquitin-dependent endocytosis; activating	S602; S720	S447	SNF1		11, 361

	dephosphorylation relays glucose signaling to transporter endocytosis; calcineurin dephosphorylation is required for Rsp5p-dependent internalization of agonist-occupied Ste2p, as part of signal desensitization; recruits Rsp5p to Ste2p via its 2 PPXY motifs; protein abundance increases in response to DNA replication stress; ROD1 has a paralog, ROG3, that arose from the whole genome duplication				
MUK1	Guanine nucleotide exchange factor (GEF); involved in vesicle-mediated vacuolar transport, including Golgi-endosome trafficking and sorting through the multivesicular body (MVB); specifically stimulates the intrinsic guanine nucleotide exchange activity of Rab family members (Vps21p/Ypt52p/Ypt53p); partially redundant with GEF VPS9; required for localization of the CORVET complex to endosomes; contains a VPS9 domain	S67; T71; T498	S67	CDC28	7, 142, 374, 379
			S245	CLB2, CDC28	7, 32, 116, 142, 373, 374, 379
DIG1	MAP kinase-responsive inhibitor of the Ste12p transcription factor; involved in the regulation of mating-specific genes and the invasive growth pathway; related regulators Dig1p and Dig2p bind to Ste12p; DIG1 has a paralog, DIG2, that arose from the whole genome duplication	S37; S395	S272	STE11	7, 32, 37, 116, 142, 217, 373, 374, 379
			S279	STE11	7, 32, 116, 142, 217, 373, 379
			S395	PKP2	7, 32, 37, 122, 142, 152, 379
HEH2	Inner nuclear membrane (INM) protein; contains helix-extension-helix (HEH) motif, nuclear localization signal sequence;	S141; S145	S123	CLB2, CDC28	142, 374, 379

	targeting to the INM requires the Srp1p-Kap95p karyopherins and the Ran cycle; HEH2 has a paralog, SRC1, that arose from the whole genome duplication					
PKH3	Protein kinase with similarity to mammalian PDK1 and yeast Pkh1p/Phk2p; yeast Pkh1p and Pkh2p are two redundant upstream activators of Pkc1p; identified as a multicopy suppressor of a pkh1 pkh2 double mutant		S834	PTK2		32, 37, 379
			T832	PTK2		32, 37, 379
STE20	Cdc42p-activated signal transducing kinase; involved in pheromone response, pseudohyphal/invasive growth, vacuole inheritance, down-regulation of sterol uptake; GBB motif binds Ste4p; member of the PAK (p21-activated kinase) family	T203; T207; T216; T408; T411; T413; S418; T546; S547; T552; S924	S206	CDC28		32, 217, 379
			S269		PSR2	32
			S502	CLB2, CDC28		7, 37, 116, 142, 290, 373, 374, 379
			S517	CDC28		32, 37, 56, 142, 370, 379
			S547	CDC28, CLN2		32, 37, 56, 116, 142, 217, 290, 370, 373, 374, 379
			S562	CDC28, CLN2		7, 32, 37, 56, 116, 142, 217, 290, 370, 373, 374, 379
			T203	CLB2, CDC28		7, 32, 142, 217, 370, 379
			T217	CTK1		32, 370, 379

			T218	PKP2	32, 379
			T511	SNF1	32, 370
			T512	CLB2, CDC28	37, 142, 370, 379
			T777	STE20	430
TCB3	Cortical ER protein involved in ER-plasma membrane tethering; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to the plasma membrane (PM) and regulate PM phosphatidylinositol-4-phosphate (PI4P) levels by controlling access of Sac1p phosphatase to its substrate PI4P in the PM; localized to the bud via specific mRNA transport; non-tagged protein detected in a phosphorylated state in mitochondria; C-termini of Tcb1p, Tcb2p and Tcb3p interact	S1335; S1340; S1342; S1346; T1347; T1350; S1354; Y1357; S1360; T1364; Y1366; S1371; S1373; T1379; T1382; S1383; S1386	S1373	CLB2, CDC28	142, 374, 379
			T1350	CDC28	7, 32, 100, 122, 142, 152, 217, 331, 370, 374, 379
SRC1	Inner nuclear membrane protein; highly enriched at telomeres and subtelomeric regions; functions in regulation of subtelomeric genes and is linked to TREX (transcription export) factors; SRC1 produces 2 splice variant proteins with different functions; alternative splicing of SRC1 pre-mRNA is promoted by Hub1p; mutant has aneuploidy tolerance; SEC1 has a paralog, HEH2, that arose from the whole genome duplication	S181	S80	CLB2, CDC28	7, 142, 217, 370, 374, 379
			S85	CLB2, CDC28	142, 152, 217, 370, 374, 379
			T241	CLB2, CDC28	7, 142, 379

			T291	CLB2, CDC28	116, 139, 142, 370, 373, 379
TAF12	Subunit (61/68 kDa) of TFIID and SAGA complexes; involved in RNA polymerase II transcription initiation and in chromatin modification, similar to histone H2A; overexpression of the human ortholog, TAF12, an oncogene involved in the formation of choroid plexus carcinomas, results in dosage chromosomal instability (dCIN) in a human cell line similar to the dCIN observed in yeast overexpressors		S325	MEC1, TEL1	7, 52, 379
NUP53	FG-nucleoporin component of central core of nuclear pore complex (NPC); also part of the NPC nuclear basket; contributes directly to nucleocytoplasmic transport; involved in regulation of transcription and mitosis; induces membrane tubulation, which may contribute to nuclear pore assembly; NUP53 has a paralog, ASM4, that arose from the whole genome duplication		S101	CDC28	7, 142, 217, 240, 370, 379
			S206	CDC28	240, 379
GIS1	Histone demethylase and transcription factor; regulates genes during nutrient limitation; activity modulated by proteasome-mediated proteolysis; has JmjC and JmjN domain in N-terminus that interact, promoting stability and proper transcriptional activity; contains two transactivating domains downstream of Jmj domains and a C-terminal DNA binding domain; relocalizes to the cytosol in response to hypoxia; GIS1 has a paralog, RPH1, that arose from the whole genome duplication	S747	S425	CDC28	7, 32, 142, 374
			S696	CDC28	7, 142, 217, 370, 374, 379

CUE4	Protein of unknown function; has a CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; CUE4 has a paralog, CUE1, that arose from the whole genome duplication	T32; S41; S48; S54	S48	KNS1	7, 32, 142, 370, 379
SEG1	Component of eisosome required for proper eisosome assembly; precedes Pil1p/Lsp1p during eisosome formation, controls eisosome length and shape; diffusely distributed, forms heterogeneous patches at plasma membrane in small buds, also found in medium and large buds; expression repressed by cAMP; similar to A. gossypii SEG gene and to S. pombe Sle1p, important for generating eisosomes; SEG1 has a paralog, SEG2, that arose from the whole genome duplication	S302; S318; S450; T452	S658	CLB2, CDC28	7, 142, 379
			S870	CDC28	142
			T675	CLB2, CDC28	7, 32, 56, 142, 370, 374, 379
YMR196W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YMR196W is not an essential gene	T1008; S1010; T1013; S1016; S1020	S1081	CDC28	7, 139, 142, 379
BUD22	Protein required for rRNA maturation and ribosomal subunit biogenesis; required for 18S rRNA maturation; also required for small ribosomal subunit biogenesis; cosediments with pre-ribosomal particles; mutation decreases efficiency of +1 Ty1 frameshifting and transposition, and affects budding pattern	T257; T283; T284; S285	T257	SNF1	7, 32, 56, 116, 139, 142, 217, 370, 373, 374, 379
MYO5	One of two type I myosin motors; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; MYO5 has a	S357; Y359; T1034; T1036; S1038; S1040; S1045; T1048; T1051	S357	YPK2	7, 32, 56, 116, 121, 122, 142, 152, 217, 370, 373, 374, 379

	paralog, MYO3, that arose from the whole genome duplication						
GAL83	One of three possible beta-subunits of the Snf1 kinase complex; allows nuclear localization of the Snf1 kinase complex in the presence of a nonfermentable carbon source; necessary and sufficient for phosphorylation of the Mig2p transcription factor in response to alkaline stress; functionally redundant with SIP1 and SIP2 for the phosphorylation of Mig1p in response to glucose deprivation; contains a glycogen-binding domain		S64	SNF1			246
			S65	SNF1			246
			S87	CKA1, CKA2, CK1B1, CKB2			246
			S93	CKA1, CKA2, CK1B1, CKB2			246
			T90	CKA1, CKA2, CK1B1, CKB2			246
RCO1	Essential component of the Rpd3S histone deacetylase complex; interacts with Eaf3p	S683	S68				7, 52, 139
TRI1	Non-essential sumoylated protein of unknown function; similar to components of human SWI/SNF complex including SMRD3; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, nucleus and nucleolus; TRI1 has a paralog, UAF30, that arose from the whole genome duplication	S113	S113	CDC28	CDC28		7, 139, 142, 379
EIS1	Component of the eisosome required for proper eisosome assembly; similar to Uso1p; authentic, non-tagged protein is detected in a phosphorylated state in highly purified	T18; S19; S23; S26; S130; S133; S151; S179; S584; S701; Y704; T706;	S23			SIW14	32, 56, 116, 142, 370, 373, 379

	mitochondria in high-throughput studies; protein increases in abundance and relocalizes from plasma membrane to cytoplasm upon DNA replication stress; EIS1 has a paralog, YKL050C, that arose from the whole genome duplication	S710; T759; T761; S762; S763; T767; S775; S780; S781; S791; S795; S825; S828; S829; S838				
			S30			SIW14	32
			S130	MCK1	SCH9		7, 32, 56, 116, 139, 142, 152, 331, 373, 374, 379
			S133	MCK1			7, 32, 56, 116, 152, 373, 379
			S136	SNF1			32, 116, 152, 373, 379
			S139	SNF1			32, 379
			S584	YPK1	TPK1		7, 32, 56, 116, 122, 139, 142, 217, 370, 373, 374, 379
			S762	PSK2		YVH1	32, 370, 374
			S763	PKP1		YVH1	7, 32, 116, 142, 152, 370, 373, 374, 379
			S775	CKA1	HRR25		7, 32, 116, 139, 142, 152, 370, 373, 379
			S791	FRK1			32
			T767	PSK2			32, 152, 379
ASM4	FG-nucleoporin component of central core of nuclear pore complex (NPC); contributes directly to nucleocytoplasmic transport; induces membrane tubulation, which may		S464	CDC28			142, 379

	contribute to nuclear pore assembly; ASM4 has a paralog, NUP53, that arose from the whole genome duplication						
MSC3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; msc3 mutants are defective in directing meiotic recombination events to homologous chromatids; potential Cdc28p substrate; protein abundance increases in response to DNA replication stress	S80; S82; S83; T144; S151; S155; Y357; S363; T646; S648; S658; S659; S660	S46	CDC28			142
RGC1	Putative regulator of the Fps1p glycerol channel; multiply phosphorylated by Hog1p under osmotic stress; contains a pleckstrin homology domain; forms homodimers and heterodimerizes with paralog Ask10p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	S1048	S969	CLB2, CDC28			142, 379
			S975	CLB2, CDC28			7, 37, 142, 379
YLR257W	Protein of unknown function; protein abundance increases in response to DNA replication stress	S66; S129; S135; S137; S139; T142; S143	S197	HOG1	PKC1	PPH21	7, 32, 116, 139, 142, 217, 370, 373, 379
			S200		CKA2	PPH21	7, 32, 56, 116, 139, 370, 373, 379
			S252	PTK1			7, 32, 370, 379
			T8	FRK1			7, 32, 142, 152, 217, 374, 379
FPR4	Peptidyl-prolyl cis-trans isomerase (PPIase); nuclear proline isomerase; affects expression of multiple genes via its role in nucleosome assembly; catalyzes isomerization of proline residues in histones H3 and H4, which affects lysine methylation of those histones; PPIase domain acts as a transcriptional	S80; S82	S80	KIN28	CKA2		7, 32, 37, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379

	repressor when tethered to DNA by lexA, and repressor activity is dependent on PPIase activity; contains a nucleoplasmin-like fold and can form pentamers						
			S82	KIN28	CKA2		7, 32, 37, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
SKG3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate; similar to Skg4p; relocalizes from bud neck to cytoplasm upon DNA replication stress; SKG3 has a paralog, CAF120, that arose from the whole genome duplication	S633	S633	SNF1			32, 56, 116, 217, 373, 379
BCP1	Essential protein involved in nuclear export of Mss4p; Mss4p is a lipid kinase that generates phosphatidylinositol 4,5-biphosphate and plays a role in actin cytoskeleton organization and vesicular transport	T205	T205		CKA2	SIT4	7, 32, 116, 139, 142, 152, 217, 370, 373, 374
ESF1	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels	S86; S372	S86	FUS3			7, 32, 116, 139, 142, 152, 217, 373, 374, 379
			S223			CMP2	7, 32, 116, 139, 142, 217, 373, 374, 379
			T220			CMP2	32, 56, 116, 139, 373, 379
VPS74	Golgi phosphatidylinositol-4-kinase effector and PtdIns4P sensor; interacts with the cytosolic domains of cis and medial	S14; T17; S18; S19; S22; S23	S14	SNF1	RIM11		7, 32, 56, 100, 139, 142, 144,

	glycosyltransferases, and in the PtdIns4P-bound state mediates the targeting of these enzymes to the Golgi; interacts with the catalytic domain of Sac1p, the major cellular PtdIns4P phosphatase, to direct dephosphosphorylation of the Golgi pool of PtdIns4P; tetramerization required for function; ortholog of human GOLPH3/GPP34/GMx33				370, 374, 379
			S19	PTK2	7, 32, 56, 100, 144, 370, 379, 402
			S23	PTK2	32, 100, 144, 370, 379
RGA2	GTPase-activating protein for polarity-establishment protein Cdc42p; implicated in control of septin organization, pheromone response, and haploid invasive growth; regulated by Pho85p and Cdc28p; RGA2 has a paralog, RGA1, that arose from the whole genome duplication	S142	S334	PHO85	372
			S380	CDC28	7, 142, 372, 379
			S733	CDC28	142, 372, 374, 379
			S763	CLB2, CDC28	7, 32, 116, 142, 152, 217, 370, 372, 373, 374, 379
			S770	CLB2, CDC28	32, 116, 142, 152, 217, 370, 372, 373, 374, 379
			S772	CLB2, CDC28	7, 116, 142, 152, 372,

						373, 374, 379
CRN1	Coronin; cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; plays a role in regulation of actin patch assembly	S456; S460; S462; S463; S465; S484; S485; T520; T565; S567; S573; T575; S578; S579; T600; S601	S463		PPH21	7, 32, 56, 116, 142, 217, 370, 373, 374, 379
RSC2	Component of the RSC chromatin remodeling complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; RSC2 has a paralog, RSC1, that arose from the whole genome duplication	S682	S682	CLB2, CDC28		7, 32, 122, 139, 142, 152, 217, 374, 379
			T11	MEC1, TEL1		52
			T243	CDC28		7, 32, 142, 374, 379
SPN1	Protein involved in RNA polymerase II transcription; is constitutively recruited to the CYC1 promoter and is required for recruitment of chromatin remodeling factors for the expression of CYC1 gene; interacts genetically or physically with RNAP II, TBP, TFIIS, and chromatin remodelling factors; central domain highly conserved throughout eukaryotes; mutations confer an Spt- phenotype	T15; S85; T86; S89; T120	S23	MEC1, TEL1		7, 32, 52, 116, 142, 152, 217, 370, 373, 374, 379
			S89	SSK2		7, 32, 56, 116, 142, 192, 217, 370, 373, 374, 379
			S118	KNS1		32, 370, 379
ATG13	Regulatory subunit of the Atg1p signaling complex; stimulates Atg1p kinase activity; required for vesicle formation during autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; contains a HORMA domain required for autophagy		S344	TPK1		142, 152, 374, 377

	and for recruitment of the phosphatidylinositol 3-kinase complex subunit Atg14p to the pre-autophagosomal structure			
		S346	TPK1	142, 152, 374, 377, 379
		S348	TOR1	7, 142, 152, 173, 174, 217, 374, 379
		S437	TOR1	32, 37, 152, 173, 174, 377
		S438	TOR1	32, 152, 173, 174
		S496	TOR1	142, 152, 173, 174
		S535	TOR1	142, 152, 173, 174
		S541	TOR1	7, 142, 152, 173
		S581	TPK1	377
		S646	TOR1	142, 152, 173, 174, 379
		S649	TOR1	7, 122, 142, 152, 173, 174, 374, 379
YCG1	Subunit of the condensin complex; required for establishment and maintenance of chromosome condensation, chromosome segregation and chromatin binding by the complex; required for tRNA genes clustering at the nucleolus; required for replication slow zone breakage following Mec1p inactivation; transcription is cell cycle regulated, peaking in mitosis and declining in G1; protein is constitutively	S16	CDC5	375

	degraded by the proteasome; rate limiting for condensin recruitment to chromatin				
			S198	CDC5	7, 142, 217, 370, 375, 379
			S902	CDC5	375
			S911	CDC5	375
			S933	CDC5	7, 52, 370, 375, 379
			S964	CDC5	375
			S981	CDC5	7, 56, 374, 375, 379
			S996	CDC5	142, 375, 379
			S1001	CDC5	375, 379
			S1008	CDC5	7, 375
			T941	CDC5	375, 379
			T949	CDC5	375, 379
			T960	CDC5	375
			T979	CDC5	7, 374, 375
VIP1	Inositol hexakisphosphate and inositol heptakisphosphate kinase; inositol heptakisphosphate (IP7) production is important for phosphate signaling; involved in cortical actin cytoskeleton function, and invasive pseudohyphal growth analogous to S. pombe asp1; inositol hexakisphosphate is also known as IP6	T143; S145	S141	MKK2	7, 32, 116, 373, 379
			S1107	CDC28	7, 32, 37, 116, 122, 142, 373, 374, 379
			S1121	PTK1	32
IMH1	Protein involved in vesicular transport; mediates transport between an endosomal compartment and the Golgi, contains a Golgi-localization (GRIP) domain that interacts with activated Arl1p-GTP to localize Imh1p to the Golgi		S825	CKA2	7, 32, 217, 370, 374, 379

NVJ2	Lipid-binding ER protein, enriched at nucleus-vacuolar junctions (NVJ); may be involved in sterol metabolism or signaling at the NVJ; contains a synaptotagmin-like-mitochondrial-lipid binding protein (SMP) domain; binds phosphatidylinositols and other lipids in a large-scale study; may interact with ribosomes, based on co-purification experiments	S591; S621; S622; T624; S640; S646	S676	CDC28		7, 122, 142, 217, 370, 379
SSK1	Cytoplasmic phosphorelay intermediate osmosensor and regulator; part of a two-component signal transducer that mediates osmosensing via a phosphorelay mechanism; required for mitophagy; dephosphorylated form is degraded by the ubiquitin-proteasome system; potential Cdc28p substrate		S195	CDC28		7, 32, 142, 379
			S673	CDC28		32, 56, 116, 142, 217, 373, 379
HBT1	Shmoo tip protein, substrate of Hub1p ubiquitin-like protein; mutants are defective for mating projection formation, thereby implicating Hbt1p in polarized cell morphogenesis; HBT1 has a paralog, YNL195C, that arose from the whole genome duplication	Y29; S41; S43; T45; S251; T259; S301; S303; Y362; S363; S427; Y428; S431; S795; S843; S850; Y855; S856; S857; S932; T939; T940; S941; Y942; S943; T948; T949; S950; S956; S959; S962; S983; S990; T991; S993; Y1003; S1005; S1036	S41	SAT4		7, 32, 116, 142, 373
			S43	PBS2		32, 116, 142, 373
			S251		SIW14	32
			S257		SIW14	32
			S301	PSK2		32, 142

			S303	MCK1			32, 142, 370, 374
			S363	PKP1		PPH22	7, 32, 56, 116, 142, 370, 373
			S561			PPH22	32, 142
			S671	CDC28		PPS1	32, 142
			S856	PKP1			32, 142
			S857	MCK1		PPH22	32, 142, 374
			S956	MCK1			7, 32, 100, 116, 142, 370, 373, 374
			S959	MCK1		PPH22	32, 100, 116, 142, 373, 374
			S962	PKP1		PPH22	32, 100, 116, 142, 373, 374
			S990	CMK1			32
			S1034	PKP1	CLA4		7, 32, 116, 122, 139, 142, 217, 373
			S1036	CLA4		PPH22	7, 32, 116, 122, 142, 373
			T366	PSK2			7, 32, 370
			T368	PKP1			32
			T949	PBS2			32
			T991	PKP1			32
			T997	MCK1			32, 56, 100, 142
			Y362	PBS2			32
			Y987	MCK1			32
VPS13	Protein involved in prospore membrane morphogenesis; peripheral membrane protein that localizes to the prospore membrane and at numerous membrane	T433; S436; T438; T440	S1715	RCK2	PKC1		7, 32, 122, 139, 142, 217, 370, 379

	contact sites; involved in sporulation, vacuolar protein sorting, prospore membrane formation during sporulation, and protein-Golgi retention; required for mitochondrial integrity; contains a PH-like domain; homologous to human CHAC and COH1 which are involved in Chorea-acanthocytosis and Cohen syndrome, respectively					
			T1379	CDC28	CDC28	7, 32, 100, 139, 142, 379
NBA1	Protein of unknown function; localizes to the bud neck and cytoplasm; interacts with Nap1p; may interact with ribosomes, based on co-purification experiments; potential Cdc28p substrate	S151; T152	S151			32, 379
			S154			32, 116, 373, 379
			S194			32, 122, 139, 142, 152, 379
			T152			32, 116, 373, 379
			T403			122, 142, 379
ZEO1	Peripheral membrane protein of the plasma membrane; interacts with Mid2p; regulates the cell integrity pathway mediated by Pkc1p and Slt2p; the authentic protein is detected in a phosphorylated state in highly purified mitochondria	S40; T49	S85	BUD32		32, 116, 152, 373
			S89	PTK1		32, 116, 152, 373, 379
			T49	VPS34		7, 32, 56, 116, 122, 139, 142, 217, 331, 370, 373, 379

ALR1	Plasma membrane Mg(2+) transporter; expression and turnover are regulated by Mg(2+) concentration; overexpression confers increased tolerance to Al(3+) and Ga(3+) ions; magnesium transport defect of the null mutant is functionally complemented by either of the human genes MAGT1 and TUSC3 that are not orthologous to ALR1	T232; S233; S236	S188		142, 379
			T143		142, 379
RTC1	Subunit of SEACAT, a subcomplex of the SEA complex; Rtc1p, along with Mtc5p and Sea4p, redundantly inhibit the TORC1 inhibitory role of the Iml1p/SEACIT (Iml1p-Npr2p-Npr3p) subcomplex, a GAP for GTPase Gtr1p (EGOC subunit) in response to amino acid limitation, thereby resulting in activation of TORC1 signaling; SEA is a coatomer-related complex that associates dynamically with the vacuole; has N-terminal WD-40 repeats and a C-terminal RING motif; null suppresses cdc13-1		S946	SNF1	7, 32, 142, 370, 379
			S950	SNF1	7, 32, 116, 142, 217, 370, 373, 379
CUE5	Ubiquitin-binding protein; functions as ubiquitin-Atg8p adaptor in ubiquitin-dependent autophagy; serves as proteaphagy receptor for inactivated 26S proteasomes; contains CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; CUE5 has a paralog, DON1, that arose from the whole genome duplication; human TOLLIP is a functional CUE-domain homolog, can complement yeast null mutant, rescuing hypersensitivity of cue5 null mutant cells to Htt-96Q	S21; S36; S45; T50; T70; S220; T346; S348; S351; T352	S21	MKK1	7, 32, 116, 142, 217, 370, 373, 379

			S220	KSP1	7, 32, 142, 217, 374, 379
			T364	CLB2, CDC28	7, 32, 100, 116, 142, 152, 217, 370, 373, 379
			T367	CDC28	32, 100, 142, 152, 370, 379
			T369	CDC28	7, 32, 152
VHS3	Negative regulatory subunit of protein phosphatase 1 Ppz1p; involved in coenzyme A biosynthesis; subunit of the phosphopantothenoylcysteine decarboxylase (PPCDC; Cab3p, Sis2p, Vhs3p) complex and the CoA-Synthesizing Protein Complex (CoA-SPC: Cab2p, Cab3p, Cab4p, Cab5p, Sis2p and Vhs3p)	T108; T183; S221; S223; T224; S225	S223	RTK1	7, 32, 142, 217
			S225	CDC28	7, 32, 142, 374
SGT1	Cochaperone protein; regulates activity of adenylyl cyclase Cyr1p; involved in kinetochore complex assembly; associates with the SCF (Skp1p/Cdc53p/F box protein) ubiquitin ligase complex; acts as a linker between Skp1p and HSP90 complexes; protein abundance increases in response to DNA replication stress	S165; S166; S168	S171	CDC28	7, 116, 142, 217, 373, 374, 379
			S361	CKA1, CKA2, CKB1, CKB2	22
GYP1	Cis-golgi GTPase-activating protein (GAP) for yeast Rabs; the Rab family members are Ypt1p (in vivo) and for Ypt1p, Sec4p, Ypt7p, and Ypt51p (in vitro); involved in vesicle docking and fusion	S87; S89	S546		7, 142, 379
			T539		7, 142, 379

			T555		142, 379
ALE1	Broad-specificity lysophospholipid acyltransferase; part of MBOAT family of membrane-bound O-acyltransferases; key component of Lands cycle; may have role in fatty acid exchange at sn-2 position of mature glycerophospholipids	S513	S513	PHO85	7, 32, 116, 122, 142, 152, 217, 373, 374, 379
HRK1	Protein kinase; implicated in activation of the plasma membrane H(+)-ATPase Pma1p in response to glucose metabolism; plays a role in ion homeostasis; protein abundance increases in response to DNA replication stress		S47	HRK1	7, 32, 116, 152, 370, 373
TCO89	Subunit of TORC1 (Tor1p or Tor2p-Kog1p-Lst8p-Tco89p); regulates global H3K56ac; TORC1 complex regulates growth in response to nutrient availability; cooperates with Ssd1p in the maintenance of cellular integrity; deletion strains are hypersensitive to rapamycin	S119; S546	S497	PTK2	32, 142, 379
			S500	PTK2	32, 142, 379
			S546	CLB2, CDC28	116, 142, 217, 373, 379
SLF1	RNA binding protein that associates with polysomes; may be involved in regulating mRNA translation; involved in the copper-dependent mineralization of copper sulfide complexes on cell surface in cells cultured in copper salts; SLF1 has a paralog, SRO9, that arose from the whole genome duplication; protein abundance increases in response to DNA replication stress	S40; S41; S42	S42	CDC28	7, 32, 122, 142, 374, 379
RCN2	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; phosphorylated in response to alpha factor; protein abundance increases in response to DNA replication stress	S102; S104; T105; S110; S129; T132; S149; S150; S152; S156; S157; S160; S183; S185; S186; S187; S188; T189; T200; S201; S204;	S143	SLT2	32

		T248; S250; S255; S257; T259				
			S150	SLT2	RIM11	7, 32, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S152	TPK2		7, 32, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S157	TPK2		7, 32, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S160	SLT2		7, 32, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			T132	TPK2		7, 32, 142, 217, 370
NUR1	Protein involved in regulation of mitotic exit; dephosphorylation target of Cdc14p in anaphase, which promotes timely rDNA segregation and allows mitotic progression; interacts with Csm1p, Lrs4p; required for rDNA repeat stability; null mutant causes increase in unequal sister-chromatid exchange; GFP-fusion protein localizes to the nuclear periphery, possible Cdc28p substrate	S417	S441	CLB2, CDC28		56, 116, 142, 373, 379

			S474	CDC28			116, 142, 189, 373, 379
			T446	CLB2, CDC28			142
RTK1	Putative protein kinase, potentially phosphorylated by Cdc28p; interacts with ribosome biogenesis factors, Cka2, Gus1 and Arc1; protein abundance increases in response to DNA replication stress	S81; S107	S60	SNF1			7, 32, 116, 370, 373, 374, 379
CHS5	Component of the exomer complex; the exomer which also contains Csh6p, Bch1p, Bch2p, and Bud7, is involved in the export of select proteins, such as chitin synthase Chs3p, from the Golgi to the plasma membrane; interacts selectively with the activated, GTP-bound form of Arf1p; Chs5p is the only protein with a BRCT domain that is not localized to the nucleus	S312; S318; S321; S338; S347; T348; S365; T373; S384; S399; S400; S579; S590; S600	S347			SIT4	32, 370
			T334			SIT4	32, 142, 370, 379
MRH1	Protein that localizes primarily to the plasma membrane; also found at the nuclear envelope; long-lived protein that is asymmetrically retained in the plasma membrane of mother cells; the authentic, non-tagged protein is detected in mitochondria in a phosphorylated state; null mutation confers sensitivity to acetic acid	S289; T295; S299	S289	YPK1	CDC28	SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
			T295	PSK2	CDC28	SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
LYS21	Homocitrate synthase isozyme; catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis	S409; T410	T410	CDC28			7, 32, 56, 116, 142, 217, 370, 373, 374

	pathway; LYS21 has a paralog, LYS20, that arose from the whole genome duplication				
DCS2	m(7)GpppX pyrophosphatase regulator; non-essential, stress induced regulatory protein; modulates m7G-oligoribonucleotide metabolism; inhibits Dcs1p; regulated by Msn2p, Msn4p, and the Ras-cAMP-cAPK signaling pathway; mutant has increased aneuploidy tolerance; DCS2 has a paralog, DCS1, that arose from the whole genome duplication	S58; S60; S63; T64; T340; S341	S63	PKH2	7, 32, 142, 370, 374
			T64	MCK1	7, 32, 116, 142, 370, 373, 374
MED2	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation; relocalizes to the cytosol in response to hypoxia	T171; T172	S208	SSN3	128, 410
MSL5	Component of commitment complex; which defines first step in splicing pathway; essential protein that interacts with Mud2p and Prp40p, forming a bridge between the intron ends; also involved in nuclear retention of pre-mRNA; relocalizes to the cytosol in response to hypoxia	S93; S95; S376; S378	S376	CDC28	7, 32, 142, 152, 370, 379
			S378	CDC28	7, 32, 142, 152, 370, 379
BUG1	Cis-golgi localized protein involved in ER to Golgi transport; forms a complex with the mammalian GRASP65 homolog, Grh1p; mutants are compromised for the fusion of ER-derived vesicles with Golgi membranes	S2; S87; T275; T277	S87	CKA2	7, 32, 116, 139, 142, 217, 370, 373, 374, 379
			T277	CDC28	142, 379
RLM1	MADS-box transcription factor; component of the protein kinase C-mediated MAP kinase pathway involved in the maintenance of cell integrity; phosphorylated and		S427	SLT2	169

	activated by the MAP-kinase Slt2p; RLM1 has a paralog, SMP1, that arose from the whole genome duplication					
			T439	SLT2		169
INP53	Polyphosphatidylinositol phosphatase; dephosphorylates multiple phosphatidylinositol phosphates; involved in trans Golgi network-to-early endosome pathway; hyperosmotic stress causes translocation to actin patches; contains Sac1 and 5-ptase domains; INP53 has a paralog, INP52, that arose from the whole genome duplication	S986; T988	S986	CDC28	PHO85	7, 32, 37, 116, 139, 142, 370, 373, 374, 379
			T988	CLB2, CDC28		7, 32, 142, 374
HER1	Protein of unknown function; required for proliferation or remodeling of the ER that is caused by overexpression of Hmg2p; may interact with ribosomes, based on co-purification experiments; HER1 has a paralog, GIP3, that arose from the whole genome duplication	S277; S280; S1013; S1204	S61	CDC28		142, 379
			T128	SNF1		32, 56, 142, 379
MAM3	Protein required for normal mitochondrial morphology; has similarity to hemolysins	S434; S435; S439; S475; T477; T485; T575; T599	S522	MCK1		32, 142
			S523	MCK1		32, 56, 142
			S527	MCK1		32, 56, 116, 142, 373, 379
			T519	MCK1		32, 56, 142, 379
HSP42	Small heat shock protein (sHSP) with chaperone activity; forms barrel-shaped oligomers that suppress unfolded protein aggregation; involved in cytoskeleton reorganization after heat shock; protein abundance increases and forms cytoplasmic foci in response to DNA replication stress	S182; S213; S214; S215; S223; S232; T236	S213	PBS2	TPK1	7, 32, 139, 142, 152, 217, 370, 379

			S214	PBS2	SNF1	PPH21	7, 32, 116, 122, 139, 142, 152, 217, 370, 373, 379
			S215			PPH21	7, 32, 116, 122, 142, 152, 217, 370, 373, 379
			S223			PPH21	7, 32, 142, 379
STB3	Ribosomal RNA processing element (RRPE)-binding protein; involved in the glucose-induced transition from quiescence to growth; restricted to nucleus in quiescent cells, released into cytoplasm after glucose repletion; binds Sin3p; relative distribution to the nucleus increases upon DNA replication stress	S9; S307	S337			PTC7	32, 142, 152, 374, 379
			S341			PTC7	32, 56, 152, 379
CMR1	Nuclear protein with a role in protein quality control; localizes to the intranuclear quality control compartment (INQ) in response to proteasome inhibition or DNA replication stress; INQ likely sequesters proteins involved in DNA metabolism for degradation or re-folding; DNA-binding protein with preference for UV-damaged DNA; contains three WD domains (WD-40 repeat); human ortholog WDR76 also exhibits perinuclear localization under similar stress conditions		S99				7, 56, 142, 379
PAR32	Protein of unknown function; hyperphosphorylated upon rapamycin treatment in a Tap42p-dependent manner; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; PAR32 is not an essential gene		S36	PHO85			7, 32, 116, 139, 142, 152, 217, 373, 374, 379

			S39	PHO85		7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S49	PHO85		32, 152
			S131	VPS15		32
			S138		YCH1	32, 142, 152, 217, 374, 379
			S141		YCH1	32, 37, 142, 152, 217, 370, 379
			S148	CLB2, CDC28		7, 32, 142, 152
			S246	CLB2, CDC28		7, 32, 116, 122, 139, 142, 152, 217, 373, 374, 379
ENT1	Epsin-like protein involved in endocytosis and actin patch assembly; functionally redundant with Ent2p; binds clathrin via a clathrin-binding domain motif at C-terminus; relocalizes from bud neck to cytoplasm upon DNA replication stress; ENT1 has a paralog, ENT2, that arose from the whole genome duplication	T160; S163	T346	PRK1		7, 56, 116, 146, 370, 373, 374, 379
			T366	PRK1		7, 142, 146, 217, 379
			T395	PRK1		7, 122, 142, 146, 152, 217, 370, 379, 421
			T415	PRK1		421
			T427	PRK1		146
CSR2	Nuclear ubiquitin protein ligase binding protein; may regulate utilization of nonfermentable carbon sources and	S1007	S963	CDC28		142

	endocytosis of plasma membrane proteins; overproduction suppresses chs5 spa2 lethality at high temp; ubiquitinated by Rsp5p, deubiquitinated by Ubp2p; CSR2 has a paralog, ECM21, that arose from the whole genome duplication						
HRP1	Subunit of cleavage factor I; cleavage factor I is a five-subunit complex required for the cleavage and polyadenylation of pre-mRNA 3' ends; RRM-containing heteronuclear RNA binding protein and hnRNPA/B family member that binds to poly (A) signal sequences; required for genome stability	S2; S87	S462	CDC28			7, 32, 116, 122, 142, 373, 379
IGO2	Protein required for initiation of G0 program; prevents degradation of nutrient-regulated mRNAs via the 5'-3' mRNA decay pathway; phosphorylated by Rim15p; GFP protein localizes to the cytoplasm and nucleus; IGO2 has a paralog, IGO1, that arose from the whole genome duplication		S119		CLA4	PPH22	32, 139, 142, 379
			S122			PPH22	32, 142, 152, 370, 379
			S128	CLB2, CDC28			32, 142, 152, 370, 379

Table 3.4 Phosphorylated proteins and their known kinases and phosphatases of high and low density cells treated with LCA on day 1.

Gene Symbol	Description	PhosphoSite in Sample	PhosphoSite in Literature	Known Kinase	Predicted Kinase	Known Phosphatases	Reference
CDC19	Pyruvate kinase; functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; regulated via allosteric activation by fructose bisphosphate; CDC19 has a paralog, PYK2, that arose from the whole genome duplication	T372; T376; S377; T378	S22	TPK1			7, 104, 122, 142, 217, 317, 370, 374, 379
			T407	CDC28			7, 142, 379
GPM1	Tetrameric phosphoglycerate mutase; mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis	S116	S116	CTK1			7, 32, 56, 122, 139, 142, 217, 370, 374, 379
RAS2	GTP-binding protein; regulates nitrogen starvation response, sporulation, and filamentous growth; farnesylation and palmitoylation required for activity and localization to plasma membrane; homolog of mammalian Ras proto-oncogenes; RAS2 has a paralog, RAS1, that arose from the whole genome duplication	S225; T226; T227	T240	SNF1			7, 32, 217, 379
HTB1	Histone H2B; core histone protein required for chromatin assembly and chromosome function; nearly identical to HTB2; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates reassembly after DNA replication, transcriptional activation, meiotic DSB formation and H3 methylation		S11	STE20			4, 2005
DPS1	Aspartyl-tRNA synthetase, primarily cytoplasmic; homodimeric enzyme that catalyzes the specific aspartylation of tRNA(Asp); class II aminoacyl tRNA synthetase; binding to its own mRNA may confer autoregulation; shares five highly conserved amino acids with human that when mutated cause leukoencephalopathy characterized by hypomyelination with brain	S2; S14; S301	S14			SIT4	7, 32, 370, 379

	stem and spinal cord involvement and leg spasticity (HBSL)						
HXK2	Hexokinase isoenzyme 2; phosphorylates glucose in cytosol; predominant hexokinase during growth on glucose; represses expression of HXK1, GLK1, induces expression of its own gene; antiapoptotic; phosphorylation/dephosphorylation at Ser14 by kinase Snf1p, phosphatase Glc7p-Reg1p regulates nucleocytoplasmic shuttling of Hxk2p; functions downstream of Sit4p in control of cell cycle, mitochondrial function, oxidative stress resistance, chronological lifespan; has paralog HXK1	S15; S158	S15	TPK1	TPK1	GLC7, REG1	7, 10, 11, 29, 32, 100, 122, 138, 139, 142, 152, 179, 190, 324, 374
			S			GLC7, REG1	-1, 10, 11, 29, 32, 100, 117, 122, 138, 139, 142, 152, 179, 190, 324, 374
HTA1	Histone H2A; core histone protein required for chromatin assembly and chromosome function; one of two nearly identical subtypes (see also HTA2); DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p; N-terminally propionylated in vivo	S129	S129	MEC1			52, 85, 100, 116, 134, 183, 379, 404, 409, 435
HTA2	Histone H2A; core histone protein required for chromatin assembly and chromosome function; one of two nearly identical (see also HTA1) subtypes; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p	S129	S129				7, 85, 116, 158, 183, 253, 379, 409, 401122
NOT3	Component of the CCR4-NOT core complex, involved in mRNA decapping; involved in transcription initiation and elongation and in mRNA degradation; conserved lysine in human homolog of Not3p and Not5p is mutated in cancers	S304; S316; T319; S324; S325; S326; S344; S347; S348; S441; S442; S446; S450; T454; S798	S450	PHO85	RIM11		7, 32, 100, 116, 139, 142, 152, 217, 373, 374, 379

			S			7, 32, 100, 116, 139, 142, 152, 217, 373, 374, 379
			T454	PHO85		7, 32, 100, 116, 142, 152, 217, 373, 374, 379
DED1	ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase; required for translation initiation of all yeast mRNAs; binds to mRNA cap-associated factors, and binding stimulates Ded1p RNA-dependent ATPase activity; mutation in human homolog DBY is associated with male infertility; human homolog DDX3X complements ded1 null mutation; DED1 has a paralog, DBP1, that arose from the whole genome duplication		S535	MCK1	SIT4	7, 32, 56, 139, 142, 152, 217, 374, 379
			S539	MCK1	SIT4	7, 32, 56, 142, 152, 217, 374, 379
			S541	MCK1		7, 32, 142, 152, 370, 379
			S543	MCK1		7, 32, 56, 142, 152, 379
			S576	MCK1		32, 56, 142, 152, 217, 379
GPH1	Glycogen phosphorylase required for the mobilization of glycogen; non-essential; regulated by cyclic AMP-mediated phosphorylation; phosphorylation by Cdc28p may coordinately regulate carbohydrate metabolism and the cell cycle; expression is	T31	T9	TPK1		222

	regulated by stress-response elements and by the HOG MAP kinase pathway					
			T27	TPK1		222, 223
			T31	TPK1		7, 32, 122, 139, 142, 154, 213, 217, 325, 326, 370, 374, 379
SNF1	AMP-activated S/T protein kinase; forms a complex with Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis; regulates nucleocytoplasmic shuttling of Hxk2p; regulates filamentous growth and acts as a non-canonical GEF, activating Arf3p during invasive growth; SUMOylation by Mms21p inhibits its function and targets Snf1p for destruction via the Slx5-Slx8 Ub ligase	T210; T408; S413	T210	ELM1	GLC7, REG1	7, 37, 92, 142, 143, 237, 250, 251, 260, 264, 284, 379, 383
TOP2	Topoisomerase II; relieves torsional strain in DNA by cleaving and re-sealing phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis; required for replication slow zone (RSZ) breakage following Mec1p inactivation; human homolog TOP2A implicated in cancers, and can complement yeast null mutant	S2; T3; T1306; T1309; T1314	S1310	KNS1		32, 116, 139, 142, 152, 217, 370, 373, 374, 379
			S1356	CKA1, CKA2		44, 108, 142, 214
			S1363	CKA1, CKA2		214
			T1250	CDC28		142, 370, 379
			T1314	KNS1	CDC28	32, 116, 139, 142, 152, 217,

						370, 373, 374, 379
			T1365	CKA1, CKA2		142, 214
URA2	Bifunctional carbamoylphosphate synthetase/aspartate transcarbamylase; catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP		S1857	TPK1		7, 56, 73, 122, 142, 217
BCY1	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA); PKA is a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation	S68; S70; S74; S77; S79; T129; S130; T131; T144; S145; S147; T150	S70	MCK1		7, 32, 142, 374, 379
			S89	CDC28		142
			S130	KNS1		7, 32, 142, 217, 370, 374
			S147	KIN4		32, 142, 374
			T129	KNS1		7, 32, 142, 217, 370, 374, 379
			T131	KNS1		7, 32, 142, 217, 370, 374, 379
			T144		CNA1	7, 32, 37, 40, 56, 142, 217, 374
CHO1	Phosphatidylserine synthase; functions in phospholipid biosynthesis; catalyzes the reaction CDP-diaclyglycerol + L-serine = CMP + L-1-phosphatidylserine, transcriptionally repressed by myo-inositol and choline	S34; T40; S46; S47; S50; T53; T54	S46	TPK1		7, 32, 59, 139, 142, 152, 217, 370, 374, 379
			S47	TPK1		7, 59, 122, 142, 152, 217, 370, 374, 379

FBP1	Fructose-1,6-bisphosphatase; key regulatory enzyme in the gluconeogenesis pathway, required for glucose metabolism; undergoes either proteasome-mediated or autophagy-mediated degradation depending on growth conditions; glucose starvation results in redistribution to the periplasm; interacts with Vid30p	S12; T13; T18	S12	TPK1	126, 142, 247, 332, 333
PRB1	Vacuolar proteinase B (yscB) with H3 N-terminal endopeptidase activity; serine protease of the subtilisin family; involved in protein degradation in the vacuole and required for full protein degradation during sporulation; activity inhibited by Pbi2p; protein abundance increases in response to DNA replication stress; PRB1 has a paralog, YSP3, that arose from the whole genome duplication		S58	SNF1	7, 32, 116, 370, 373, 379
			S60	SNF1	32
RPS6A; RPS6B	Protein component of the small (40S) ribosomal subunit; homologous to mammalian ribosomal protein S6, no bacterial homolog; phosphorylated on S233 by Ypk3p in a TORC1-dependent manner, and on S232 in a TORC1/2-dependent manner by Ypk1/2/3p; RPS6B has a paralog, RPS6A, that arose from the whole genome duplication		S232	YPK3	7, 32, 100, 116, 122, 142, 152, 162, 373, 379
SEC7	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors; involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles	S2; T334; S434; S437; S439; S809; T1722; S1723; S1726; S1804	S780	VPS34	7, 32, 142, 217, 374, 379
			S782	VPS34	32, 142, 379
			T1240	CDC28	139, 142, 217, 379
SCH9	AGC family protein kinase; functional ortholog of mammalian S6 kinase; phosphorylated by Tor1p and required for	S288; S289; S290	S711	TOR1	32, 142, 152, 217,

	TORC1-mediated regulation of ribosome biogenesis, translation initiation, and entry into G0 phase; involved in transactivation of osmostress-responsive genes; regulates G1 progression, cAPK activity and nitrogen activation of the FGM pathway; integrates nutrient signals and stress signals from sphingolipids to regulate lifespan				335, 379, 406
			S726	TOR1	7, 32, 37, 116, 142, 152, 217, 335, 373, 374, 379, 406
			S758	TOR1	176, 335, 406
			S765	TOR1	176, 335, 406
			T570	PKH1	7, 37, 46, 150, 176, 275, 315, 335, 370, 379, 406, 415
			T723	TOR1	32, 142, 152, 176, 217, 335, 379, 406
			T737	TOR1	46, 176, 275, 335, 379, 406
CAF20	Phosphoprotein of the mRNA cap-binding complex; involved in translational control; repressor of cap-dependent translation initiation; competes with eIF4G for binding to eIF4E	S91; T99; T101; T102; T104; S105; T106; T111	S58	PSK2	342
			S59	PSK2	342
			S78	FRK1	32, 116, 142, 152, 373, 379

			S91	SLT2	CKA2	7, 32, 116, 139, 142, 217, 370, 373, 374, 379, 452
			S			7, 32, 116, 139, 142, 217, 370, 373, 374, 379, 452
			T102	SLT2		7, 32, 116, 122, 142, 217, 370, 373, 374, 379
KIN1	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; KIN1 has a paralog, KIN2, that arose from the whole genome duplication	S660; S663; S764; S937; S938	S660	SNF1		7, 32, 142, 379
			S663	SNF1		7, 32, 142, 370, 379
KIN2	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; KIN2 has a paralog, KIN1, that arose from the whole genome duplication		S24	CDC28, CLB2		7, 37, 142, 379
			S609	CDC28		7, 37, 142, 217, 379
			S643	CDC28		7, 32, 37, 116, 142, 370, 373, 374, 379
PCT1	Cholinephosphate cytidylyltransferase; a rate-determining enzyme of the CDP-choline pathway for phosphatidylcholine synthesis, inhibited by Sec14p, activated upon lipid-binding; contains an element within the regulatory domain involved in both silencing and activation of enzymatic activity	S346; T349	S346	MKK1		7, 32, 122, 139, 142, 217, 374, 379

DPM1	Dolichol phosphate mannose (Dol-P-Man) synthase of ER membrane; catalyzes formation of Dol-P-Man from Dol-P and GDP-Man; required for biosynthesis of glycosyl phosphatidylinositol (GPI) membrane anchor, as well as O-mannosylation and protein N- and O-linked glycosylation; human homolog DPM1 can complement yeast mutant strains		S141	TPK1		21
ABF1	DNA binding protein with possible chromatin-reorganizing activity; involved in transcriptional activation, gene silencing, and DNA replication and repair	S467; S720	S193	MEC1, TEL1		7, 32, 142, 370, 379
			S720	CKA1, CKA2, CKB1, CKB2	CKA2	7, 56, 116, 139, 142, 217, 373, 374, 379, 405
			S			7, 116, 139, 142, 217, 373, 374, 379, 405
YAK1	Serine-threonine protein kinase; component of a glucose-sensing system that inhibits growth in response to glucose availability; upon nutrient deprivation Yak1p phosphorylates Pop2p to regulate mRNA deadenylation, the co-repressor Crf1p to inhibit transcription of ribosomal genes, and the stress-responsive transcription factors Hsf1p and Msn2p; nuclear localization negatively regulated by the Ras/PKA signaling pathway in the presence of glucose	S38; T288; Y530	Y530	YAK1		7, 13, 122, 142, 152, 175, 217, 374, 379
NSP1	FG-nucleoporin component of central core of the nuclear pore complex; also part of the nuclear pore complex (NPC) nuclear basket; contributes directly to nucleocytoplasmic transport and maintenance of the NPC permeability barrier; found in stable complex with Nup82p, Gle2p and two other FG-		S361	RAD53		7, 370, 379

	nucleoporins (Nup159p and Nup116p); also found in stable complex with Nic96p and two other FG-nucleoproteins (Nup49p and Nup57p)				
CYC8	General transcriptional co-repressor; acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters; can form the prion [OCT+]	S421; T426; S429; S741; S768; S815; S817; S943	S780	MEC1, TEL1	7, 370
			S815	KNS1	7, 32, 142, 217, 370, 374, 379
			S819	KNS1	32, 142, 379
ABP1	Actin-binding protein of the cortical actin cytoskeleton; important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; inhibits barbed-end actin filament elongation; phosphorylation within its Proline-Rich Regio, mediated by Cdc28p and Pho85p, protects Abp1p from proteolysis mediated by its own PEST sequences; mammalian homolog of HIP-55 (hematopoietic progenitor kinase 1 [HPK1]-interacting protein of 55 kDa)	T157; S163; T165; S167; S169; S174; T181; S183; S313; S475; S478; S481	S26	PTK2	32
			S169	CDC28, CLB2	7, 32, 56, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S183	CDC28	7, 32, 56, 100, 116, 142, 152, 217, 370, 373, 374, 379
			S313	CDC28	7, 32, 116, 142, 373, 379

			T30	PTK2		32
			T31	PTK2		32
			T165	CDC28, CLB2	PHO85	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			T			7, 32, 56, 100, 122, 139, 142, 152, 374, 379
			T181	CDC28, CLB2	PHO85	7, 32, 56, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
			T			7, 32, 56, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
HSP26	Small heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation; long-lived protein that is preferentially retained in mother cells and forms cytoplasmic foci; oligomer activation requires heat-induced conformational change; also has mRNA binding activity	S2; S5; T42; S47; T48; S208; S211	S208	MEC1, TEL1		7, 52, 100, 142, 152, 379
			S211	MEC1, TEL1		7, 52, 100, 122, 139, 142, 152, 374, 379
VMA2	Subunit B of V1 peripheral membrane domain of vacuolar H+-ATPase; electrogenic	T501; S503; S504; S511; S515	S503	SNF1		7, 32, 56, 370, 374

	proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the cytoplasm; protein abundance increases in response to DNA replication stress; human homolog ATP6V1B1, implicated in autosomal-recessive distal renal tubular acidosis (RTA) with sensorineural deafness, complements yeast null mutant						
			S511	MEC1, TEL1	CKA2		7, 116, 139, 142, 152, 217, 370, 373, 374, 379
			S				7, 116, 139, 142, 152, 217, 370, 373, 374, 379
PDA1	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex; catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA; phosphorylated; regulated by glucose; PDH complex is concentrated in spots within the mitochondrial matrix, often near the ERMES complex and near peroxisomes	Y309; S313; S315	S313	PKP1, PKP2	CKA2		7, 32, 56, 100, 110, 122, 139, 142, 152, 217, 258, 331, 370, 374, 379
			S				7, 32, 56, 100, 110, 122, 139, 142, 152, 217, 258, 331, 370, 374, 379
OM45	Mitochondrial outer membrane protein of unknown function; major constituent of the outer membrane, extending into the intermembrane space; interacts with porin (Por1p) and with Om14p; imported via the presequence pathway involving the TOM and	T207	T207		SNF1	PPH22	7, 32, 139, 379

	TIM23 complexes, then assembled in the outer membrane by Mim1p; protein abundance increases in response to DNA replication stress						
			T			PPH22	7, 32, 139, 379
APA1	AP4A phosphorylase; bifunctional diadenosine 5',5'''-P1,P4-tetraphosphate phosphorylase and ADP sulfurylase involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; catalyzes phosphorolysis of dinucleoside oligophosphates, cleaving substrates' alpha/beta-anhydride bond and introducing Pi into the beta-position of the corresponding NDP formed; protein abundance increases under DNA replication stress; APA1 has a paralog, APA2, that arose from the whole genome duplication	T60; T75	T60	KNS1			7, 32, 142, 217, 370, 379
PFK1	Alpha subunit of heterooctameric phosphofructokinase; involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes	S166; S179; S188; S189; S192	S3	MEC1, TEL1	CKA2		7, 52, 139, 379
			S				7, 52, 139, 379
PFK2	Beta subunit of heterooctameric phosphofructokinase; involved in glycolysis; indispensable for anaerobic growth; activated by fructose-2,6-bisphosphate and AMP; mutation inhibits glucose induction of cell cycle-related genes	S36; S41; S42; S47; T48; S148; T149; T152; S160; S163; S166; S167; S171; Y172; T173; Y177	S166	SNF1			7, 32, 116, 142, 152, 217, 370, 373, 379
			S167	SNF1			7, 32, 116, 142, 152, 217, 370, 373, 379
			S171	SNF1	CKA2		7, 32, 56, 100, 116, 122, 139, 142, 152,

					217, 370, 373, 374, 379
			S		7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S652	PKC1	81
			Y172	SNF1	7, 32, 139
SEC2	Guanyl-nucleotide exchange factor for the small G-protein Sec4p; essential for post-Golgi vesicle transport and for autophagy; associates with the exocyst, via exocyst subunit Sec15p, on secretory vesicles	S632; S740	S515	SNF1	7, 32, 116, 139, 142, 152, 217, 373, 374, 379
CBF1	Basic helix-loop-helix (bHLH) protein; forms homodimer to bind E-box consensus sequence CACGTG present at MET gene promoters and centromere DNA element I (CDEI); affects nucleosome positioning at this motif; associates with other transcription factors such as Met4p and Isw1p to mediate transcriptional activation or repression; associates with kinetochore proteins, required for chromosome segregation; protein abundance increases in response to DNA replication stress	T138; S140; S149	S45	MEC1, TEL1	7, 32, 52, 116, 142, 152, 370, 373, 379
			S48	MEC1, TEL1	7, 32, 52, 116, 142, 152, 370, 373, 379
			S155	SSN3	32, 142, 370, 379
			S156	SSN3	7, 32, 142, 217, 370, 379

			T138	SSN3	CDC28	7, 32, 139, 142, 217, 379
			T			7, 32, 139, 142, 217, 379
			T154	CTK1		7, 32, 116, 142, 370, 373, 379
PHO81	Cyclin-dependent kinase (CDK) inhibitor; regulates Pho80p-Pho85p and Pcl7p-Pho85p cyclin-CDK complexes in response to phosphate levels; inhibitory activity for Pho80p-Pho85p requires myo-D-inositol heptakisphosphate (IP7) generated by Vip1p; relative distribution to the nucleus increases upon DNA replication stress	S542; S543	S956	RAD53		7, 52
STE4	G protein beta subunit; forms a dimer with Ste18p to activate mating signaling pathway, forms heterotrimer with Gpa1p and Ste18p to dampen signaling; pheromone-induced phosphorylation plays critical role in chemotropism; may recruit Rho1p to polarized growth site during mating; contains WD40 repeats		S335	FUS3		216, 370, 379
			T320	FUS3		216, 379
YPK2	Protein kinase similar to S/T protein kinase Ypk1p; functionally redundant with YPK1 at the genetic level; participates in a signaling pathway required for optimal cell wall integrity; involved in the TORC-dependent phosphorylation of ribosomal proteins Rps6a/b (S6); human homolog SGK2 can complement a ypk1 ypk2 double mutant	T63; T66	S641			142, 172, 217
			T501			7, 37, 46, 142, 172, 217, 370, 379
			T659			46, 142, 172

FPR1	Peptidyl-prolyl cis-trans isomerase (PPIase); binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; N-terminally propionylated in vivo; mutation is functionally complemented by human FKBP1A	S45; S46; S51	S51	PSK2	7, 32, 142, 370, 379
SUI2	Alpha subunit of the translation initiation factor eIF2; eIF2 is involved in identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; protein abundance increases in response to DNA replication stress	S292; S294; S301	S52	GCN2	76, 374, 387, 411, 459
			S292	CKA1, CKA2, CKB1, CKB2	7, 98, 100, 116, 142, 152, 373, 374, 379, 411
			S294	CKA1, CKA2, CKB1, CKB2	7, 98, 100, 116, 142, 152, 373, 374, 379, 411
			S301	CKA1, CKA2, CKB1, CKB2	7, 98, 100, 116, 142, 152, 373, 374, 379, 411
MCK1	Dual-specificity ser/thr and tyrosine protein kinase; roles in chromosome segregation, meiotic entry, genome stability, phosphorylation-dependent protein degradation (Rcn1p and Cdc6p), inhibition of protein kinase A, transcriptional regulation, inhibition of RNA pol III, calcium stress and inhibition of Clb2p-Cdc28p after nuclear division; MCK1 has a paralog, YGK3, that arose from the whole genome duplication	S24; S27; T30; S196; S198; Y199; S202	Y199	MCK1	7, 32, 142, 152, 217, 328, 374, 379

SIN3	Component of both the Rpd3S and Rpd3L histone deacetylase complexes; involved in transcriptional repression and activation of diverse processes, including mating-type switching and meiosis; involved in the maintenance of chromosomal integrity	T303; T304; T308	S316	CDC28			7, 32, 100, 142, 217, 374, 379
			S1126	MEC1, TEL1			52
			T304	CDC28			7, 32, 142, 217, 374, 379
HSP12	Plasma membrane protein involved in maintaining membrane organization; involved in maintaining organization during stress conditions; induced by heat shock, oxidative stress, osmostress, stationary phase, glucose depletion, oleate and alcohol; protein abundance increased in response to DNA replication stress and dietary restriction; regulated by the HOG and Ras-Pka pathways; required for dietary restriction-induced lifespan extension		S21	MEC1, TEL1		PTC6	7, 32, 52, 56, 116, 142, 370, 373, 379
			S24	PKP1		PTC6	7, 32, 56, 116, 142, 370, 373, 379
			S59	PKP1			7, 32, 116, 142, 370, 373, 379
			S73	PKP1			7, 32, 116, 139, 142, 370, 373, 379
			S87	PKP1			7, 32, 370
			Y25	PKP1			32, 142
SPA2	Component of the polarisome; functions in actin cytoskeletal organization during polarized growth; acts as a scaffold for Mkk1p and Mpk1p cell wall integrity signaling components; potential Cdc28p	S605; S606	S254	CLB2, CDC28	CDC28		7, 32, 56, 116, 122, 139, 142, 217, 373, 374, 379

substrate; coding sequence contains length polymorphisms in different strains; SPA2 has a paralog, SPH1, that arose from the whole genome duplication					
	S274	CLB2, CDC28			7, 32, 116, 142, 373
	S585	CLB2, CDC28		SIW14	7, 32, 56, 116, 122, 139, 142, 152, 217, 370, 373, 379
	S599	CDC28	CDC28		7, 32, 122, 139, 142, 152, 217, 370, 379
	S646	CLB2, CDC28			7, 116, 142, 217, 373
	S883	CDC28			7, 116, 142, 217, 373, 374, 379
	S910	CDC28			7, 116, 142, 217, 370, 373, 374, 379
	S937	CLB2, CDC28			56, 116, 142, 217, 373, 379
	S961	CLB2, CDC28			7, 32, 56, 142, 217, 370, 374, 379
	S979	CLB2, CDC28			7, 32, 142, 217, 370, 379
	S1080	CLB2, CDC28			116, 122, 142, 370, 373, 379
	S1087	CDC28			116, 142, 373, 379

TAF2	TFIID subunit (150 kDa); involved in RNA polymerase II transcription initiation	S318	T19			7, 142, 370
GSY1	Glycogen synthase; expression induced by glucose limitation, nitrogen starvation, environmental stress, and entry into stationary phase; GSY1 has a paralog, GSY2, that arose from the whole genome duplication; relocalizes from nucleus to cytoplasmic foci upon DNA replication stress	S651; S655	S651	MCK1	RIM11	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S			7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S655	MCK1	PHO85	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S			7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
MBR1	Protein involved in mitochondrial functions and stress response; overexpression suppresses growth defects of hap2, hap3, and hap4 mutants; MBR1 has a paralog, ISF1, that arose from the whole genome duplication	S222; S224; S226; S227	S69			142
STE11	Signal transducing MEK kinase; involved in pheromone response and pseudohyphal/invasive growth pathways where it phosphorylates Ste7p, and the high		S281	STE20		86

	osmolarity response pathway, via phosphorylation of Pbs2p; regulated by Ste20p and Ste50p; protein abundance increases in response to DNA replication stress					
			S285	STE20		86
			T286	STE20		86
SSD1	Translational repressor with a role in polar growth and wall integrity; regulated by Cbk1p phosphorylation to effect bud-specific translational control and localization of specific mRNAs; interacts with TOR pathway components; contains a functional N-terminal nuclear localization sequence and nucleocytoplasmic shuttling appears to be critical to Ssd1p function	S480; S481; T482; S487; S489; S491; S492; T494	S42	CBK1		156, 217
			S126	CBK1		32, 142, 152, 156
			S152	CBK1		32, 142, 156, 374, 379
			S164	CBK1		32, 56, 142, 156, 217, 370, 374
			S228	CBK1		32, 142, 156
			S231	CDC28		7, 32, 142, 156, 370
			S267	CLB2, CDC28	CDC28	7, 32, 139, 142, 152
			S			7, 32, 139, 142, 152
			S286	CDC28		7, 32, 142, 152, 156, 374, 379
			S293	CKB1		32, 142, 156
			S319	CKB1		156
			S492	CDC28		7, 32, 100, 116, 142, 217, 370,

						373, 374, 379
			T261	CBK1		156
UBP1	Ubiquitin-specific protease; removes ubiquitin from ubiquitinated proteins; cleaves at the C terminus of ubiquitin fusions irrespective of their size; capable of cleaving polyubiquitin chains	S555; S638; S755	S530	CKA1	CKA2	7, 32, 100, 116, 139, 142, 152, 217, 373, 379
			S			7, 32, 100, 139, 142, 152, 217, 379
			S531	CKA1	CKA2	7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 379
			S			7, 32, 100, 116, 139, 142, 152, 217, 373, 379
NAP1	Histone chaperone; involved in histone exchange by removing and replacing histone H2A-H2B dimers or histone variant dimers from assembled nucleosomes; involved in the transport of H2A and H2B histones to the nucleus; required for the regulation of microtubule dynamics during mitosis; interacts with mitotic cyclin Clb2p; controls bud morphogenesis; phosphorylated by CK2; protein abundance increases in response to DNA replication stress	T20; T24	S159	CKA1, CKA2, CKB1, CKB2		43
			S177	CKA1, CKA2, CKB1, CKB2	CKA2	7, 32, 37, 43, 116, 139, 142, 152, 217, 370, 373, 379

			S			7, 32, 37, 43, 116, 139, 142, 152, 217, 370, 373, 379
			S397	CKA1, CKA2, CKB1, CKB2		43
			T20	PTK2		7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
			T24	PTK2		7, 32, 37, 116, 122, 142, 152, 217, 373, 374, 379
FEN1; ELO2	Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; ELO2 has a paralog, ELO1, that arose from the whole genome duplication; lethality of the elo2 elo3 double null mutation is functionally complemented by human ELOVL1 and weakly complemented by human ELOVL3 or ELOV7	T334; S336; S338	S336	MCK1	PHO85	7, 32, 56, 100, 139, 142, 152, 217, 370, 374, 379
			S			7, 32, 56, 100, 139, 142, 152, 217, 370, 374, 379
			S338	MCK1		7, 32, 56, 100, 142, 152, 217,

							370, 374, 379
			T334	MCK1	PHO85		7, 32, 56, 100, 139, 142, 152, 217, 370, 374, 379
			T				7, 32, 56, 100, 139, 142, 152, 217, 370, 374, 379
USO1	Essential protein involved in vesicle-mediated ER to Golgi transport; binds membranes and functions during vesicle docking to the Golgi; required for assembly of the ER-to-Golgi SNARE complex		S1032	RAD53			7, 370, 379
RPC53	RNA polymerase III subunit C53	S119; S224; T228; T232; S234	S224	MCK1			7, 32, 56, 116, 142, 152, 204, 217, 370, 373, 374, 379
			T228	MCK1			32, 56, 116, 122, 142, 152, 204, 217, 370, 373, 374, 379
			T232	MCK1			7, 32, 56, 116, 122, 142, 152, 204, 217, 373, 374, 379
HSP30	Negative regulator of the H(+)-ATPase Pma1p; stress-responsive protein; hydrophobic plasma membrane localized; induced by heat shock, ethanol treatment,	S308; T331	S308		CDC28	SIT4	7, 32, 100, 139, 142, 370, 379

	weak organic acid, glucose limitation, and entry into stationary phase					
			S		SIT4	7, 32, 100, 139, 142, 370, 379
PWP2	Conserved 90S pre-ribosomal component; essential for proper endonucleolytic cleavage of the 35 S rRNA precursor at A0, A1, and A2 sites; contains eight WD-repeats; PWP2 deletion leads to defects in cell cycle and bud morphogenesis	S232	S664	MEC1, TEL1		7, 52, 139, 142
CDC48	AAA ATPase; subunit of polyUb-selective segregase complex involved in ERAD, INM-associated degradation (INMAD), mitotic spindle disassembly, macroautophagy, PMN, ribosome-associated degradation, ribophagy, homotypic ER membrane fusion, SCF complex disassembly, cell wall integrity during heat stress, and telomerase regulation; mobilizes membrane-anchored transcription factors by regulated Ub/proteasome-dependent processing (RUP); human ortholog VCP complements a cdc48 mutant	S770	S770	MPS1		7, 32, 37, 56, 142, 217, 370, 374, 379
			T735	MPS1		7, 37, 139, 142, 370, 379
PPZ1	Serine/threonine protein phosphatase Z, isoform of Ppz2p; involved in regulation of potassium transport, which affects osmotic stability, cell cycle progression, and halotolerance		S49		OCA1	32, 142, 217, 379
			S142	CDC28		142, 217, 379
			S265	CLB2, CDC28		142, 217, 379
			T261	CLB2, CDC28		142, 217, 379
CDC60	Cytosolic leucyl tRNA synthetase; ligates leucine to the appropriate tRNA; human homolog LARS can complement yeast	T142; T152	T142	CDC28		116, 142, 373

	temperature-sensitive mutant at restrictive temperature					
RFA2	Subunit of heterotrimeric Replication Protein A (RPA); RPA is a highly conserved single-stranded DNA binding protein involved in DNA replication, repair, and recombination; RPA protects against inappropriate telomere recombination, and upon telomere uncapping, prevents cell proliferation by a checkpoint-independent pathway; in concert with Sgs1p-Top2p-Rmi1p, stimulates DNA catenation/decatenation activity of Top3p; protein abundance increases in response to DNA replication s		S27	IME2		7, 62, 345
			S122	IME2		7, 25, 52, 56, 113, 116, 122, 139, 142, 217, 373, 374, 379
GSY2	Glycogen synthase; expression induced by glucose limitation, nitrogen starvation, heat shock, and stationary phase; activity regulated by cAMP-dependent, Snf1p and Pho85p kinases as well as by the Gac1p-Glc7p phosphatase; GSY2 has a paralog, GSY1, that arose from the whole genome duplication; relocalizes from cytoplasm to plasma membrane upon DNA replication stress	S651; S655	S651	MCK1	RIM11	7, 32, 37, 100, 122, 133, 139, 142, 148, 149, 152, 217, 342, 370, 374, 379, 427
			S			7, 32, 37, 100, 122, 133, 139, 142, 148, 152, 217, 370, 374, 379
			S655	PCL10, PHO85		7, 26, 37, 100, 122, 133, 142,

					148, 149, 217, 342, 370, 374, 379, 427
			T668	PCL10, PHO85	26, 133, 148, 149, 427
SPT5	Spt4p/5p (DSIF) transcription elongation factor complex subunit; the Spt4/5 complex binds to ssRNA in a sequence-specific manner, and in concert with RNAP I and II has multiple roles regulating transcriptional elongation, RNA processing, quality control, and transcription-coupled repair; interacts with DNA upstream of RNAPII and the non-template strand of the transcription bubble; Spt5p is the only transcription elongation factor conserved in all domains of life	T40	S931	BUR2, SGV1	227
			S937	BUR2, SGV1	227
			S948	BUR2, SGV1	227
			S958	BUR2, SGV1	227
			S969	BUR2, SGV1	227
			S975	BUR2, SGV1	227
			S981	BUR2, SGV1	227
			S987	BUR2, SGV1	227
			S1000	BUR2, SGV1	227
			S1009	BUR2, SGV1	227, 379
			S1015	BUR2, SGV1	142, 227, 379
			S1032	BUR2, SGV1	142, 152, 227, 379

			S1043	BUR2, SGV1		152, 227, 379
			S1052	BUR2, SGV1		142, 227, 379
			S1058	BUR2, SGV1		152, 227, 379
MIG1	Transcription factor involved in glucose repression; sequence specific DNA binding protein containing two Cys2His2 zinc finger motifs; regulated by the SNF1 kinase and the GLC7 phosphatase; regulates filamentous growth along with Mig2p in response to glucose depletion; activated in stochastic pulses of nuclear localization, shuttling between cytosol and nucleus depending on external glucose levels and its phosphorylation state	S278	S222	SNF1		32, 77, 142, 152, 367, 428
			S264	CLB2, CDC28		32, 142, 152, 379
			S278	SNF1		7, 32, 77, 142, 152, 299, 367, 379, 396, 428
			S311	SNF1		6, 7, 77, 122, 142, 152, 217, 299, 307, 370, 379, 396, 428
			S381	SNF1		7, 77, 142, 367, 428
FUN19	Non-essential protein of unknown function; expression induced in response to heat stress; FUN19 has a paralog, YOR338W, that arose from the whole genome duplication	T194; S207; S267; S269	S207	CDC28	PHO85	7, 139, 142
			S			7, 139, 142
			S211	CDC28		7, 142
BMH1	14-3-3 protein, major isoform; controls proteome at post-transcriptional level, binds	T231; T234; S235; S238; S240	S238	HRR25		32, 63, 142, 374, 417

	proteins and DNA, involved in regulation of exocytosis, vesicle transport, Ras/MAPK and rapamycin-sensitive signaling, aggresome formation, spindle position checkpoint; protein increases in abundance and relative distribution to the nucleus increases upon DNA replication stress; antiapoptotic gene similar to human 14-3-3; BMH1 has a paralog, BMH2, that arose from whole genome duplication					
BEM1	Protein containing SH3-domains; involved in establishing cell polarity and morphogenesis; functions as a scaffold protein for complexes that include Cdc24p, Ste5p, Ste20p, and Rsr1p	S458	S72			7, 32, 131, 370, 379, 401
			S458		SNF1	7, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
MCM2	Protein involved in DNA replication; component of the Mcm2-7 hexameric helicase complex that binds chromatin as a part of the pre-replicative complex; relative distribution to the nucleus increases upon DNA replication stress	T547	S107	CDC7		323
			S164	CDC7		39, 142, 310, 311, 323, 376
			S170	CDC7		39, 142, 310, 311, 323, 376
NTH1	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; phosphorylated and activated by Cdc28p at the G1/S phase transition to coordinately regulate carbohydrate metabolism and the cell cycle; inhibited by Dcs1p; NTH1 has a	S83	S20	TPK1		7, 100, 104, 122, 142, 217, 370, 379, 423

	paralog, NTH2, that arose from the whole genome duplication					
			S66	CDC28		7, 32, 56, 100, 104, 142, 152, 370, 374, 379, 423
			S83	TPK1		7, 32, 56, 100, 104, 142, 152, 370, 374, 379, 423
PUP2	Alpha 5 subunit of the 20S proteasome; involved in ubiquitin-dependent catabolism; human homolog is subunit zeta	T55; S56; S251	S56	CDC28		7, 122, 142, 181, 217, 370, 374, 379
CDC3	Component of the septin ring that is required for cytokinesis; septins are GTP-binding proteins that assemble with other septins into rod-like complexes that can associate with other rods to form filament polymers; septin rings at the mother-bud neck act as scaffolds for recruiting factors needed for cell division and as barriers to prevent diffusion of specific proteins between mother and daughter cells	S2; S9	S498	CTK1		32, 379
			S503	CLB2, CDC28		32, 116, 122, 142, 152, 373, 374, 379, 389
			S509	CLB2, CDC28		7, 32, 37, 116, 142, 152, 217, 373, 374, 379, 389
HOG1	Mitogen-activated protein kinase involved in osmoregulation; controls global reallocation of RNAPII during osmotic shock; mediates recruitment/activation of RNAPII at Hot1p-	Y176; T179	T174	PBS2	PTC2, PTC3	7, 18, 30, 32, 37, 100, 139, 142, 152, 241,

	dependent promoters; binds calmodulin; stimulates antisense transcription to activate CDC28; defines novel S-phase checkpoint with Mrc1p that prevent replication/transcription conflicts; nuclear form represses pseudohyphal growth; autophosphorylates; protein abundance increases under DNA replication stress					352, 379, 408, 420
			Y176	PBS2	PTC1	7, 18, 30, 32, 100, 139, 142, 152, 241, 352, 379, 408, 420
NIP1	eIF3c subunit of the eukaryotic translation initiation factor 3 (eIF3); involved in the assembly of preinitiation complex and start codon selection; eIF3 is also involved in programmed stop codon readthrough	S98; S99; S103; S222; T228; T239	S98	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
			S99	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
			S103	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
NUP2	Nucleoporin involved in nucleocytoplasmic transport; binds to either the nucleoplasmic or cytoplasmic faces of the nuclear pore complex depending on Ran-GTP levels; also has a role in chromatin organization	T14; S17; S20; S84; S203; S205; S537; S538; S540; T577; S581	S17	MCK1		7, 32, 56, 100, 116, 142, 152, 217, 369, 373, 374, 379
			S20	MCK1		7, 32, 56, 100, 116, 142, 152, 217, 369,

						373, 374, 379
			S68	RAD53		7, 139, 142, 370
			S203	RAD53	PTP1	7, 32, 56, 116, 142, 152, 217, 370, 373, 374
			S205	ALK2	PTP1	7, 32, 56, 116, 142, 152, 217, 370, 373, 374
			S248	RAD53		7, 370
			S284	RAD53		7, 370
			S317	RAD53		7, 370
			S351	RAD53		7, 52, 370
			S368	RAD53		7, 142, 370, 379
			S399	MEC1, TEL1		370, 379
			S512	RAD53		370
			S523	RAD53		370
PAN1	Part of actin cytoskeleton-regulatory complex Pan1p-Sla1p-End3p; associates with actin patches on cell cortex; promotes protein-protein interactions essential for endocytosis; binds to and activates Arp2/3 complex in vitro; phosphorylation of Thr-1225 is regulated by MAPK Hog1p in response to osmotic stress; previously thought to be a subunit of poly(A) ribonuclease	T570; T993; S1003; S1250; S1253; S1255; T1256	T148	PRK1		147, 395, 453
			T170	PRK1		147, 395, 453
			T194	PRK1		147, 395, 453
			T221	PRK1		395, 453

			T241	PRK1		7, 147, 395, 453
			T398	PRK1		147, 395, 453
			T415	PRK1		147, 395, 453
			T428	PRK1		147, 395, 453
			T452	PRK1		147, 395, 453
			T473	PRK1		147, 395, 453
			T504	PRK1		147, 395, 453
			T513	PRK1		147, 395, 453
			T544	PRK1		147, 395, 453
			T551	PRK1		147, 395, 453
			T566	PRK1		7, 146
			T570	PRK1		7, 32, 142, 147, 152, 379, 395, 453
ZUO1	Ribosome-associated chaperone; zuotin functions in ribosome biogenesis and as a chaperone for nascent polypeptide chains in partnership with Ssz1p and SSb1/2; contains a DnaJ domain and functions as a J-protein partner for Ssb1p and Ssb2p; human gene DNAJC2 can partially complement yeast zuo1 null mutant		S50		CMP2	7, 32, 56, 100, 142, 152, 217, 370, 374, 379
PAH1	Mg2+-dependent phosphatidate (PA) phosphatase; dephosphorylates PA to yield diacylglycerol; regulates phospholipid synthesis, nuclear/ER membrane growth, lipid droplet formation, triacylglycerol synthesis, vacuolar homeostasis and cell wall integrity; phosphorylated by Pho85p/Pho80p,	T163; T164; S166; T170; T175; T176; S814	S110		NEM1, SPO7	58, 60, 289

	Cdc28p/Cyclin B, PKA, PKC, and CKII, regulating activity, localization, and proteosomal degradation; homolog of mammalian lipins 1 and 2; human homologs LPIN1, LPIN2, LPIN3 complement the null					
			S114		NEM1, SPO7	58, 60, 289
			S168		NEM1, SPO7	58, 60, 116, 289, 373, 379
			S602	CDC28	NEM1, SPO7	7, 58, 60, 142, 217, 289, 379
			S744		NEM1, SPO7	7, 58, 60, 116, 142, 152, 217, 289, 373, 374, 379
			S748		NEM1, SPO7	7, 58, 60, 116, 122, 142, 152, 217, 289, 373, 374, 379
			T723		NEM1, SPO7	58, 60, 289
SIP1	Alternate beta-subunit of the Snf1p kinase complex; may confer substrate specificity; vacuolar protein containing KIS (Kinase-Interacting Sequence) and ASC (Association with Snf1 kinase Complex) domains involved in protein interactions	S331	S198	CDC28		142, 217, 379
			S200	CDC28		7, 116, 142, 217, 373, 374, 379
IME2	Serine/threonine protein kinase involved in activation of meiosis; associates with Ime1p and mediates its stability, activates Ndt80p; IME2 expression is positively regulated by Ime1p; human CDK2 can complement ime2 null mutant	T33; S35; S48	T242			37, 346, 347

			Y244				346, 347, 20543984
SRP40	Nucleolar serine-rich protein; role in preribosome assembly or transport; may function as a chaperone of small nucleolar ribonucleoprotein particles (snoRNPs); immunologically and structurally to rat Nopp140	S133; T141	S133			SIW14	32, 56, 116, 152, 373
STH1	ATPase component of the RSC chromatin remodeling complex; required for expression of early meiotic genes; promotes base excision repair in chromatin; essential helicase-related protein homologous to Snf2p	S51; S52; S1188	S1172	MEC1, TEL1	CKA2		7, 52
			S				52
			T1166	MEC1, TEL1	CKA2		7, 52, 139
			T				7, 52, 139
SLA1	Cytoskeletal protein binding protein; required for assembly of the cortical actin cytoskeleton; interacts with proteins regulating actin dynamics and proteins required for endocytosis; found in the nucleus and cell cortex; has 3 SH3 domains	S794; T797; S799; T831; T834; T835	S437	CLB2, CDC28			7, 32, 142, 152, 370, 374, 379
			S449			PSR2	7, 32, 116, 142, 217, 373, 379
YSC84	Actin-binding protein; involved in bundling of actin filaments and endocytosis of actin cortical patches; activity stimulated by Las17p; contains SH3 domain similar to Rvs167p; YSC84 has a paralog, LSB3, that arose from the whole genome duplication	Y296; S301	S311				7, 32, 142, 217, 374, 379
UGP1	UDP-glucose pyrophosphorylase (UGPase); catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; involved in PKA-mediated oxidative stress resistance and long-term survival in stationary phase; UGP1 has a		S11	PSK2			7, 32, 37, 56, 100, 116, 122, 142, 217, 342, 368, 373, 374, 379

	paralog, YHL012W, that arose from the whole genome duplication					
CBF5	Pseudouridine synthase catalytic subunit of box H/ACA snoRNPs; acts on large and small rRNAs, on snRNA U2, and on some mRNAs; mutations in human ortholog dyskerin cause the disorder dyskeratosis congenita; small nucleolar ribonucleoprotein particles are also known as snoRNPs	T378; S398	S395	MEC1, TEL1	RIM11	7, 32, 52, 116, 139, 142, 373, 374, 379
			S399	MEC1, TEL1		7, 32, 52, 116, 142, 370, 373, 374, 379
			T396	FRK1	CKA2	7, 32, 139, 142
PPZ2	Serine/threonine protein phosphatase Z, isoform of Ppz1p; involved in regulation of potassium transport, which affects osmotic stability, cell cycle progression, and halotolerance	T298; S299; S310; S314; S315; S317; S359; S362	S299	CLB2, CDC28		7, 142, 374, 379
			S310	CLB2, CDC28		7, 37, 142, 374, 379
SLA2	Adaptor protein that links actin to clathrin and endocytosis; involved in membrane cytoskeleton assembly and cell polarization; present in the actin cortical patch of the emerging bud tip; dimer in vivo		S308	CDC28		7, 32, 100, 142, 152, 217, 374, 379
			T290	SSK2		7, 32, 142, 217, 370, 374, 379
			T294	CDC28		7, 32, 100, 122, 142, 217, 370, 374, 379
			T296	CDC28		7, 32, 100, 122, 142, 217, 370, 374, 379
			T298	CDC28		7, 32, 100, 142, 152,

						217, 370, 374, 379
PGM1	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; PGM1 has a paralog, PGM2, that arose from the whole genome duplication	T111; T118; S120; S513	S120	FRK1		7, 32, 116, 122, 142, 152, 217, 370, 373, 374, 379
MKS1	Pleiotropic negative transcriptional regulator; involved in Ras-CAMP and lysine biosynthetic pathways and nitrogen regulation; involved in retrograde (RTG) mitochondria-to-nucleus signaling	S440; S442	S217	FRK1		7, 32, 139
TGL1	Steryl ester hydrolase; one of three gene products (Yeh1p, Yeh2p, Tgl1p) responsible for steryl ester hydrolase activity and involved in sterol homeostasis; localized to lipid particle membranes	S462; S466; S538	S466	CDC28		142, 379
			S492	TPK3		7, 32, 142, 370, 374, 379
EDE1	Scaffold protein involved in the formation of early endocytic sites; putative regulator of cytokinesis; homo-oligomerization is required for localization to and organization of endocytic sites; has a network of interactions with other endocytic proteins; binds membranes in a ubiquitin-dependent manner; may also bind ubiquitinated membrane-associated proteins; interacts with Cmk2 and functions upstream of CMK2 in regulating non-apoptotic cell death; homolog of mammalian Eps15	S241; S931; S1006; S1008; S1011; S1012; T1065; S1093; S1095; S1096; S1100; S1104; T1160; T1178; S1179; S1181; S1187; T1307; S1309	S241		PTC4	7, 32, 100, 122, 142, 152, 217, 370, 374, 379
			S244		PTC4	7, 32, 100, 122, 142, 152, 217, 374, 379
			S249		PTC4	7, 32, 142, 152, 217, 374, 379

			S527		PSR2	32, 152, 370
			S1069		CMP2	7, 32, 142, 379
			S1096	FUS3		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			S1100	PHO85		7, 32, 56, 100, 116, 142, 152, 217, 370, 373, 374, 379
			T238	CDC28		7, 142, 217, 379
			T1072		CMP2	7, 32, 142, 379
PIN4	Protein involved in G2/M phase progression and response to DNA damage; interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage	T512; S538; S541; S545; S653; S655	S466	CDC28		7, 32, 116, 122, 139, 142, 217, 373, 374, 379
			S541	CDC28		32, 122, 142, 152, 379
			S653		SIT4	7, 32, 37, 116, 122, 142, 370, 373, 374, 379
			S655		SIT4	7, 32, 116, 122, 142, 370, 373, 374, 379
SHP1	UBX domain-containing substrate adaptor for Cdc48p; ubiquitin regulatory X domain-containing protein that acts as a substrate	S97; S106; T107; S115; S224; S315; S321; S322; T331	S106	KNS1		7, 32, 100, 116, 152, 373, 379

	recruiting cofactor for Cdc48p; positively regulates Glc7p PPase activity to promote growth and mitotic progression in complex with Cdc48p; ubiquitinated protein interactor involved in ER-associated degradation (ERAD); regulated by nuclear Ub-dependent degradation (INMAD pathway) independent of the Asi and Doa10 complexes; homolog of human p47 (NSFL1C)					
			S108	PTK1		7, 32, 100, 116, 152, 370, 373, 379
			S315	CDC28	CDC28	7, 32, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S			7, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S322	CDC28		7, 32, 139, 142, 217, 374, 379
FAB1	1-phosphatidylinositol-3-phosphate 5-kinase; vacuolar membrane kinase that generates phosphatidylinositol (3,5)P2, which is involved in vacuolar sorting and homeostasis	S1710; S1712	T183			7, 142, 370
TSA1	Thioredoxin peroxidase; acts as both ribosome-associated and free cytoplasmic antioxidant; self-associates to form high-molecular weight chaperone complex under oxidative stress; chaperone activity essential for growth in zinc deficiency; required for telomere length maintenance; binds and modulates Cdc19p activity; protein	T167; T174; T179; T183; S187	T174	FRK1		7, 32, 116, 142, 373, 379

	abundance increases, forms cytoplasmic foci during DNA replication stress; TSA1 has a paralog, TSA2, that arose from the whole genome duplication					
GCS1	ADP-ribosylation factor GTPase activating protein (ARF GAP); involved in ER-Golgi transport; required for prospore membrane formation; regulates phospholipase Spo14p; shares functional similarity with Glo3p; GCS1 has a paralog, SPS18, that arose from the whole genome duplication	S149; T151; S157; T161; S168; T170	S157	CKA1		7, 32, 142, 217, 370, 374, 379
			T151	MCK1		32, 142, 152, 217
			T161	CDC28		7, 32, 139, 142, 217, 370, 374, 379
			T170	CLB2, CDC28		7, 32, 100, 142, 370, 379
DEF1	RNAPII degradation factor; forms a complex with Rad26p in chromatin, enables ubiquitination and proteolysis of RNAPII present in an elongation complex; mutant is deficient in Zip1p loading onto chromosomes during meiosis	T258; S260; S307	S273	RAD53		56, 116, 370
BDF1	Protein involved in transcription initiation; functions at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p; BDF1 has a paralog, BDF2, that arose from the whole genome duplication	S270; S612; S613; S615; T617	S630	MEC1, TEL1		52, 379
SWH1	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats and FFAT motif; interacts with ER anchor Scs2p at the nucleus-vacuole junction; regulated by sterol binding; SWH1 has a paralog, OSH2,	T432; S442; T443; S488; S490; S492; S678; S683; T694; S732; T1053; S1056	S1056	SNF1	SNF1	7, 32, 139, 142, 370, 379

	that arose from the whole genome duplication						
			S				7, 32, 139, 370, 379
			T1053	SNF1	SNF1		7, 32, 139, 370, 379
			T				7, 32, 139, 370, 379
SIS2	Negative regulatory subunit of protein phosphatase 1 (Ppz1p); involved in coenzyme A biosynthesis; subunit of phosphopantothenoylcysteine decarboxylase (PPCDC: Cab3p, Sis2p, Vhs3p) complex and the CoA-Synthesizing Protein Complex (CoA-SPC: Cab2p, Cab3p, Cab4p, Cab5p, Sis2p and Vhs3p); SIS2 has a paralog, VHS3, that arose from the whole genome duplication	T119; S121; S124; S130; S132	S47	CDC28			7, 32, 142, 217, 370, 374, 379
			S56	CDC28			7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
EAP1	eIF4E-associated protein, competes with eIF4G for binding to eIF4E; accelerates mRNA degradation by promoting decapping, facilitated by interaction with eIF4E; essential for Puf5p mediated repression; associates with Puf5p and Dhh1p; inhibits cap-dependent translation; functions independently of eIF4E to maintain genetic stability; plays a role in cell growth, implicated in the TOR signaling cascade	S389; S390; T391	S363			PSR1	32, 142
			S387	MCK1			7, 32
ELF1	Transcription elongation factor with a conserved zinc finger domain; implicated in the maintenance of proper chromatin structure in actively transcribed regions;	S124; S142	S117	PSK2			7, 32, 116, 142, 193, 217, 370, 373, 374, 379

	deletion inhibits Brome mosaic virus (BMV) gene expression					
			S124	PSK2		7, 32, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
SPC42	Central plaque component of spindle pole body (SPB); involved in SPB duplication, may facilitate attachment of the SPB to the nuclear membrane	T357; T359	T357	MPS1		37, 142, 379
YKR018C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; protein abundance increases in response to DNA replication stress; YKR018C has a paralog, IML2, that arose from the whole genome duplication	T184; S185; S187; S192; T193; T196; T199; S246; S375; S377; S380	S380	PKH2		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
GPT2	Glycerol-3-phosphate/dihydroxyacetone phosphate sn-1 acyltransferase; located in lipid particles and the ER; involved in the stepwise acylation of glycerol-3-phosphate and dihydroxyacetone in lipid biosynthesis; the most conserved motifs and functionally relevant residues are oriented towards the ER lumen	S631; S632; S668; S671; T692; S693	T692	YPK1	CKA2	7, 32, 122, 139, 142, 370, 374, 379
			T			7, 32, 139, 142, 374, 379
TGL4	Multifunctional lipase/hydrolase/phospholipase; triacylglycerol lipase, steryl ester hydrolase, and Ca2+-independent phospholipase A2; catalyzes acyl-CoA dependent acylation of LPA to PA; required with Tgl3p for timely bud formation; phosphorylated and activated by Cdc28p; TGL4 has a paralog, TGL5, that arose from the whole genome duplication		S756	CDC28		7, 142
			S890	CDC28		56, 195

			T675	CLB2, CDC28		7, 142, 195
PGM2	Phosphoglucomutase; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; functions as the acceptor for a Glc-phosphotransferase; protein abundance increases in response to DNA replication stress; PGM2 has a paralog, PGM1, that arose from the whole genome duplication	T111; T117; S119; S512	S119	RAD53		7, 32, 116, 122, 142, 370, 373, 374, 379
STV1	Subunit a of the vacuolar-ATPase V0 domain; one of two isoforms (Stv1p and Vph1p); Stv1p is located in V-ATPase complexes of the Golgi and endosomes while Vph1p is located in V-ATPase complexes of the vacuole	S223; S228	S223	CTK1		7, 32, 122, 142, 152, 217, 370, 374, 379
VRP1	Verprolin, proline-rich actin-associated protein; involved in cytoskeletal organization and cytokinesis; promotes actin nucleation and endocytosis; related to mammalian Wiskott-Aldrich syndrome protein (WASP)-interacting protein (WIP)	S519; S522; S703; S709	S709	CDC28		32, 142, 379
YRO2	Protein with a putative role in response to acid stress; null mutant is sensitive to acetic acid; transcription is regulated by Haa1p and induced in the presence of acetic acid; protein observed in plasma membrane foci in the presence of acetic acid; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies	T341; S343	S297		SIW14	32, 142
			S299		SIW14	7, 32, 142, 370, 379
AKL1	Ser-Thr protein kinase; member (with Ark1p and Prk1p) of the Ark kinase family; involved in endocytosis and actin cytoskeleton organization	S407; S504; S541	S504	CLB2, CDC28		7, 32, 56, 142, 152, 374, 379

			S801	CLB2, CDC28		7, 37, 116, 142, 217, 373, 379
			S1072	AKL1		7, 32, 34, 142, 152, 217, 338, 370, 374, 379
BAP2	High-affinity leucine permease; functions as a branched-chain amino acid permease involved in uptake of leucine, isoleucine and valine; contains 12 predicted transmembrane domains; BAP2 has a paralog, BAP3, that arose from the whole genome duplication	S16; S24	S16	CDC28		7, 142, 370, 374, 379
ECM21	Protein involved in regulating endocytosis of plasma membrane proteins; identified as a substrate for ubiquitination by Rsp5p and deubiquitination by Ubp2p; promoter contains several Gcn4p binding elements; ECM21 has a paralog, CSR2, that arose from the whole genome duplication	S18; T20; S136; S140; S306; T959; S962; S1027; T1028; S1030	S33	CLB2, CDC28		32, 116, 142, 373, 379
			S550	DUN1		7, 52
			S1030	CDC28		7, 142, 152, 308, 379
			T1028	CDC28		7, 142, 152, 379
HEK2	RNA binding protein involved in asymmetric localization of ASH1 mRNA; represses translation of ASH1 mRNA, an effect reversed by Yck1p-dependent phosphoryation; regulates telomere position effect and length; similarity to hnRNP-K	S252; S358; S360; S362	S252		YVH1	7, 32, 301, 370, 374, 379
			S358	YCK1		7, 56, 142, 217, 301, 370, 374
			S360	YCK1		7, 142, 217, 301, 370, 374
			S362	YCK1		7, 142, 301, 370, 379

			S381	YCK1	301
			T352	YCK1	301
			T355	YCK1	301
NCL1	S-adenosyl-L-methionine-dependent tRNA: m5C-methyltransferase; methylates cytosine to m5C at several positions in tRNAs and intron-containing pre-tRNAs; increases proportion of tRNALeu(CAA) with m5C at wobble position in response to hydrogen peroxide, causing selective translation of mRNA from genes enriched in TTG codon; loss of NCL1 confers hypersensitivity to oxidative stress; similar to Nop2p and human proliferation associated nucleolar protein p120	T415; S423; S424; S431; T664; T665; S667; T671; T673; T675; S676; T677	S424	MKK2	7, 32, 116, 142, 373, 374, 379
			T426	CDC28	7, 32, 142, 379
IST2	Cortical ER protein involved in ER-plasma membrane tethering; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to the plasma membrane (PM) and regulate PM phosphatidylinositol-4-phosphate (PI4P) levels by controlling access of Sac1p phosphatase to its substrate PI4P in the PM; localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process	T701; S704; T712; S714; T726; S729; Y730; T736; S757; S763; S764; S767; S768; S844; S847; T850; T853	S764	CTK1	32, 374
			S767	YPK1	7, 32, 374, 379
SDS24	Protein involved in cell separation during budding; one of two S. cerevisiae homologs (Sds23p and Sds24p) of the S. pombe Sds23 protein, which is implicated in APC/cyclosome regulation; may play an indirect role in fluid-phase endocytosis; protein abundance increases in response to DNA replication stress; SDS24 has a paralog, SDS23, that arose from the whole genome duplication	T90; T92; S94; S98; S404; T441; S447; S458	S94	CTK1	7, 32, 56, 116, 142, 373, 379

			S458	CDC28		7, 142, 217, 370, 374, 379
TPS3	Regulatory subunit of trehalose-6-phosphate synthase/phosphatase; involved in synthesis of storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway; TPS3 has a paralog, TSL1, that arose from the whole genome duplication	S51; S52; T55; S56; S58; S59; Y61; S148; S150; S154; S181; S195	S148	CDC28		7, 32, 122, 142, 152, 217, 374, 379
TSL1	Large subunit of trehalose 6-phosphate synthase/phosphatase complex; Tps1p-Tps2p complex converts uridine-5'-diphosphoglucose and glucose 6-phosphate to trehalose; contributes to survival to acute lethal heat stress; mutant has aneuploidy tolerance; protein abundance increases in response to DNA replication stress; TSL1 has a paralog, TPS3, that arose from the whole genome duplication	S49; S53; S56; S71; S73; S77; S79; S85; S86; T87; T88; T115; S118; S135; S137; S138; S147; S155; S157; S161; S186; T191; S192; T194; S195; T205; T215; S216; T219; S220	S49	CKA1		7, 32, 122, 142, 379
			S77	CDC28	CDC28	7, 32, 100, 122, 139, 142, 370, 374, 379
			S			7, 32, 100, 122, 139, 142, 370, 374, 379
			S79	MCK1		7, 32, 142, 370
			S135	CDC28	CDC28	7, 32, 139, 142, 370, 374
			S			7, 32, 139, 142
			S147	CDC28	CDC28	7, 32, 139, 142, 370, 374, 379

			S				7, 32, 139, 142, 370, 374, 379
			S155	MCK1			32, 142
			S157	MCK1			32
			S161	CDC28	CDC28		7, 32, 122, 139, 142, 374, 379
			S				7, 32, 122, 139, 142, 374, 379
LEO1	Component of the Paf1 complex; which associates with RNA polymerase II and is involved in histone methylation; plays a role in regulating Ty1 transposition; involved in transcription elongation as demonstrated by the G-less-based run-on (GLRO) assay	S132; S358; S372; T374	S34	MEC1, TEL1			370
			S132			CMP2	7, 32, 116, 142, 217, 373, 379
			S339	MEC1, TEL1			52, 370, 379
RCK2	Protein kinase involved in response to oxidative and osmotic stress; identified as suppressor of S. pombe cell cycle checkpoint mutations; similar to CaM (calmodulin) kinases; RCK2 has a paralog, RCK1, that arose from the whole genome duplication	S186; S187	S46	CDC28			7, 32, 56, 116, 122, 142, 152, 370, 373, 374, 379
			S520	HOG1			31, 159, 391
			T379	HOG1			391
RFC1	Subunit of heteropentameric Replication factor C (RF-C); RF-C is a DNA binding protein and ATPase that acts as a clamp loader of the proliferating cell nuclear antigen (PCNA) processivity factor for DNA polymerases delta and epsilon	S40; S79; S80; T82; S88	T48	CLB2, CDC28			142, 379
SIC1	Cyclin-dependent kinase inhibitor (CKI); inhibitor of Cdc28-Clb kinase complexes that controls G1/S phase transition, preventing premature S phase and ensuring genomic	S191	S69				33, 188, 262, 283, 287, 295, 414

integrity; phosphorylated by Clb5/6-Cdk1 and Cln1/2-Cdk1 kinase which regulate timing of Sic1p degradation; phosphorylation targets Sic1p for SCF(CDC4)-dependent turnover; functional homolog of mammalian Kip1			
	S76		33, 188, 261, 262, 283, 287, 295, 414, 441
	S80		37, 188, 262, 283, 414
	S145		37, 97, 122, 283, 295, 354, 414
	S191		7, 32, 37, 116, 122, 139, 142, 152, 272, 283, 373, 374, 414
	S201		7, 23, 37, 61, 64, 65, 116, 139, 142, 217, 374, 379
	T2	CDC28	33, 139, 283, 287, 295, 414
	T5		7, 139, 283, 287, 414
	T33		37, 97, 262, 283, 287, 354, 413, 414
	T45		37, 97, 262, 354, 379

			T48			33, 261, 262, 283, 295, 354, 414
			T173			7, 32, 90, 97, 116, 122, 152, 217, 272, 273, 283, 295, 373, 414, 461
KIC1	Protein kinase of the PAK/Ste20 family, required for cell integrity; physically interacts with Cdc31p (centrin), which is a component of the spindle pole body; part of the RAM network that regulates cellular polarity and morphogenesis		S735	CLB2, CDC28		7, 142, 374, 379
CIC1	Essential protein that interacts with proteasome components; has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles	S365; S366	S5	MCK1		32, 100, 370
			S7	MCK1		32, 100, 370
			S10	MCK1		7, 32, 100, 116, 370, 373
			S17	MCK1	PSR1	32, 116, 370, 373, 379
			T11	MCK1	PSR1	7, 32, 100, 116, 370, 373, 379
			T15	MCK1		32, 116, 373, 379
RSC30	Component of the RSC chromatin remodeling complex; non-essential gene required for regulation of ribosomal protein genes and the cell wall/stress response; null mutants are osmosensitive; RSC30 has a paralog, RSC3, that arose from the whole genome duplication	S150; S152	S815	MEC1, TEL1		52

YHR097C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus; YHR097C has a paralog, PAL1, that arose from the whole genome duplication	S221; S222; T223; T224; T225; S233	S222			YVH1	7, 32, 100, 116, 217, 370, 373, 379
			S315	PTK1			7, 32, 56, 116, 142, 152, 373, 379
			T313			PPQ1	7, 32, 116, 142, 152, 373, 379
BZZ1	SH3 domain protein implicated in regulating actin polymerization; able to recruit actin polymerization machinery through its SH3 domains; colocalizes with cortical actin patches and Las17p; interacts with type I myosins	S472	S472	SNF1			7, 32, 142, 374, 379
KEL1	Protein required for proper cell fusion and cell morphology; forms a complex with Bud14p and Kel2p that regulates Bnr1p (formin) to affect actin cable assembly, cytokinesis, and polarized growth; functions in a complex with Kel2p to negatively regulate mitotic exit, interacts with Tem1p and Lte1p; localizes to regions of polarized growth; potential Cdc28p substrate	S503; S613; S691; Y700; S704; S742; S748; T755; T1001; S1003	S67	CLB2, CDC28			7, 32, 116, 122, 142, 373, 374, 379
			S503	CDC28			7, 116, 142, 373, 379
			S613	CDC28	CDC28		7, 37, 116, 122, 139, 142, 217, 370, 373, 374, 379
			S				7, 37, 116, 122, 139, 142, 217, 370, 373, 374, 379

			S689	CDC28			7, 116, 142, 217, 370, 373, 374, 379
NVJ1	Nuclear envelope protein; anchored to the nuclear inner membrane, that interacts with the vacuolar membrane protein Vac8p to promote formation of nucleus-vacuole junctions during piecemeal microautophagy of the nucleus (PMN)	S156; S182; T187; S188; S190; S199; T251; S285; S290	S250	SNF1	CKA2		32, 139, 370, 379
			S				32, 139, 370, 379
			S298	CDC28			7, 116, 142, 217, 373, 379
			T251	SNF1			7, 32, 142, 370, 374, 379
FPR3	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; affects expression of multiple genes via its role in nucleosome assembly; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; PPIase domain acts as a transcriptional repressor when tethered to DNA by lexA, and repressor activity is dependent on PPIase activity; FPR3 has a paralog, FPR4, that arose from the whole genome duplication		S80	KSP1		CMP2	7, 32, 37, 116, 142, 152, 217, 373, 433
			S81	KSP1		CMP2	7, 32, 37, 116, 142, 152, 217, 373
			S186	CKA1, CKA2			426
			T89	SSK2			32, 142
			Y184	CKA1, CKA2, CKB1, CKB2		MSG5	243, 425, 426

BFR1	Component of mRNP complexes associated with polyribosomes; involved in localization of mRNAs to P bodies; implicated in secretion and nuclear segregation; multicopy suppressor of BFA (Brefeldin A) sensitivity		T336	CDC28	7, 122, 139, 142, 217, 293, 370, 373, 374
SEC31	Component of the Sec13p-Sec31p complex of the COPII vesicle coat; COPII coat is required for vesicle formation in ER to Golgi transport; mutant has increased aneuploidy tolerance	T996; S997; S999	S836	CDC28	7, 116, 122, 142, 373, 379
			S974	RAD53	7, 100, 142, 370, 374, 379
			S980	CDC28	7, 32, 100, 142, 374, 379
			S988	KIN82	32, 142, 379
			S992	KIN82	7, 32, 100, 139, 142, 217, 374, 379
HAL5	Putative protein kinase; overexpression increases sodium and lithium tolerance, whereas gene disruption increases cation and low pH sensitivity and impairs potassium uptake, suggesting a role in regulation of Trk1p and/or Trk2p transporters; HAL5 has a paralog, KKQ8, that arose from the whole genome duplication		S64	CDC28	142, 152
			S229	MCK1	32
			S233	MCK1	7, 32, 142, 374, 379
TEM1	GTP-binding protein of the Ras superfamily; involved in termination of M-phase; controls actomyosin and septin dynamics during cytokinesis	S236; S240	S240	CDC28	139, 142, 152, 379
MSS4	Phosphatidylinositol-4-phosphate 5-kinase; involved in actin cytoskeleton organization and cell morphogenesis; multicopy suppressor of stt4 mutation	T659; S661	S225	PTK1	32, 142, 152, 374, 379

			T222	PTK1		32, 37, 142, 152, 217, 374, 379
UME6	Rpd3L histone deacetylase complex subunit; key transcriptional regulator of early meiotic genes; involved in chromatin remodeling and transcriptional repression via DNA looping; binds URS1 upstream regulatory sequence, represses transcription by recruiting conserved histone deacetylase Rpd3p (through co-repressor Sin3p) and chromatin-remodeling factor Isw2p; couples metabolic responses to nutritional cues with initiation and progression of meiosis, forms compl	S316; S318; S321; T403	S107	MCK1, MRK1, RIM11		32, 142, 379, 436
			S316	FRK1		7, 32, 142, 152, 217, 379
			T99	MCK1, MRK1, RIM11		32, 142, 244, 379, 436
			T103	MCK1, MRK1, RIM11		32, 379, 436
AKR1	Palmitoyl transferase involved in protein palmitoylation; acts as a negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; contains ankyrin repeats; AKR1 has a paralog, AKR2, that arose from the whole genome duplication; any of several human homologs encoding DHHC-type zinc fingers (ZDHHC) can complement temperature sensitivity of yeast akr1 null mutant	S51; S57	S57	TPK3	CKA1	7, 32, 116, 139, 142, 152, 217, 370, 373, 379
			S			7, 32, 139, 142, 152, 217, 370, 379
YCF1	Vacuolar glutathione S-conjugate transporter; ABC-C transporter of the ATP-binding	S251; S869; S872; S903	S251	CKA1, CKA2		7, 56, 116, 139, 142,

	cassette family; required for vacuole fusion; forms stable complexes with vacuole fusion machinery; regulates Vam7p recruitment to vacuoles; role in detoxifying metals (Cd, Hg, As); transports GSSG that is not immediately reduced in cytosol to vacuole; transports unconjugated bilirubin, selenodigluthatione, oxidized glutathione; similar to human cystic fibrosis protein CFTR						302, 303, 313, 370, 373, 379
			S908	TPK1			7, 88, 139, 142, 152, 217, 302, 370, 374, 379, 382
CAT8	Zinc cluster transcriptional activator; necessary for derepression of a variety of genes under non-fermentative growth conditions, active after diauxic shift, binds carbon source responsive elements; relative distribution to the nucleus increases upon DNA replication stress	S173	S562	SNF1			48
YMR124W; EPO1	Protein involved in septin-ER tethering; interacts with ER membrane protein, Scs2p, and Shs1p, a septin ring component, at bud neck to create ER diffusion barrier; GFP-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; interacts with Crm1p in two-hybrid assay; YMR124W has a paralog, YLR031W, that arose from the whole genome duplication	Y355; S356	S586	CLB2, CDC28			142, 379
TIF4631	Translation initiation factor eIF4G; subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); interacts with Pab1p and with eIF4A (Tif1p); also has a role in biogenesis of the large ribosomal subunit; TIF4631 has a paralog, TIF4632, that arose from the whole genome duplication	S163; S191; S194; S195; S232; T241; T242; T276	S522	KSP1		SIW14	32, 152, 379
TIF4632	Translation initiation factor eIF4G; subunit of the mRNA cap-binding protein complex		T196	CDC28	CDC28		7, 116, 139, 142, 217,

	(eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); TIF4632 has a paralog, TIF4631, that arose from the whole genome duplication				370, 373, 374, 379
			T		7, 116, 139, 142, 370, 373, 374, 379
			T301	CDC28	142, 217
RPH1	JmjC domain-containing histone demethylase; targets tri- and dimethylated H3K36; associates with actively transcribed regions and promotes elongation; repressor of autophagy-related genes in nutrient-replete conditions; damage-responsive repressor of PHR1; phosphorylated by the Rad53p-dependent DNA damage checkpoint pathway and by a Rim1p-mediated event during starvation; target of stress-induced hormesis; RPH1 has a paralog, GIS1, that arose from the whole genome duplication	S459; S557; S561; S688; S689	S139	RAD53	52
			S430	CDC28	7, 32, 139, 142, 152, 379
			S561	CDC28	7, 32, 116, 142, 152, 217, 373, 379
			S575	CDC28	7, 142, 379
BEM2	Rho GTPase activating protein (RhoGAP); involved in the control of cytoskeleton organization and cellular morphogenesis; required for bud emergence; potential GAP for Rho4p		T1038	CDC28	142, 379
BOI2	Protein implicated in polar growth, functionally redundant with Boi1p; interacts with bud-emergence protein Bem1p; contains an SH3 (src homology 3) domain and a PH (pleckstrin homology) domain; BOI2 has a	T372; S373; S375; S666; S667	S450	CDC28	32, 142, 217

	paralog, BOI1, that arose from the whole genome duplication					
			S457	CDC28		32, 142, 217
			S519	CDC28	CDC28	7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 374, 379
			S			7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 374, 379
			S523	CDC28	CDC28	7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 374, 379
			S			7, 32, 56, 116, 139, 142, 152, 217, 373, 374, 379
			S652	CLB2, CDC28		122, 142, 217, 374, 379
GTT3	Protein of unknown function may be involved in glutathione metabolism; function suggested by computational analysis of large-scale protein-protein interaction data; N- and C-terminal fusion proteins localize to the cell periphery	S116; T120; S121; T123	S116	CTK1		32, 142, 217, 370, 374, 379
ZRG8	Protein of unknown function; authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; GFP-fusion protein is localized to the	S676	S365			32, 56

	cytoplasm; transcription induced under conditions of zinc deficiency						
			S914				142, 379
YER079W	Putative protein of unknown function	T31; S39; S41; Y186; S189; S192; S194; S197; T201	S39		RIM11	SIT4	7, 32, 139, 142, 374
			S			SIT4	7, 32, 139, 142
			S41	CDC28		SIT4	7, 32, 142, 374, 379
			S189	TPK3			7, 32, 142, 370, 379
			S192	TPK3			7, 32, 142, 370, 379
			S194	CKA1			7, 32, 142, 379
			T53			SIT4	32
SCS2	Integral ER membrane protein, regulates phospholipid metabolism; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to plasma membrane (PM) and regulate PI4P levels by controlling access of Sac1p phosphatase to substrate PI4P in the PM; interacts with FFAT motifs in Opi1p, Swh1p, Osh2p, and Osh3p; involved in telomeric silencing; VAP homolog; SCS2 has a paralog, SCS22, that arose from the whole genome duplication	T204	T204	CLB2, CDC28			32, 139, 142, 379
BUR6	Subunit of a heterodimeric NC2 transcription regulator complex; complex binds to TBP and can repress transcription by preventing preinitiation complex assembly or stimulate activated transcription; homologous to human NC2alpha; complex also includes Ncb2p; bur6 ncb2 double mutation is functionally complemented by coexpression of human DRAP1 and DR1, although the single bur6 mutation is not complemented by its ortholog DRAP1	S141	T64				66, 139

SOK1	Protein of unknown function; overexpression suppresses the growth defect of mutants lacking protein kinase A activity; involved in cAMP-mediated signaling; localized to the nucleus; similar to the mouse testis-specific protein PBS13	S193; S197	S191	CDC28			7, 142, 374, 379
			S193	CDC28			7, 116, 142, 373, 374, 379
YTA7	Protein that localizes to chromatin; has a role in regulation of histone gene expression; has a bromodomain-like region that interacts with the N-terminal tail of histone H3, and an ATPase domain; relocalizes to the cytosol in response to hypoxia; potentially phosphorylated by Cdc28p	S11; S1142	S1142	MEC1, TEL1	CKA2		7, 32, 37, 52, 116, 139, 142, 369, 370, 373, 374, 379
			S				7, 32, 37, 52, 116, 139, 142, 369, 370, 373, 374, 379
PFK26	6-phosphofructo-2-kinase; inhibited by phosphoenolpyruvate and sn-glycerol 3-phosphate; has negligible fructose-2,6-bisphosphatase activity; transcriptional regulation involves protein kinase A	S42; S43; S667; S671; S673; S674; S675	S652	TPK1			7, 139, 142, 217, 370, 379
			T157	TPK1			7, 56, 82, 142, 217, 370, 379
VHS2	Regulator of septin dynamics; involved in the regulation of septin dynamics at bud neck after mitotic entry, likely by stabilizing septin structure; regulated at post-translational level by cell cycle dependent phosphorylation; likely phosphorylated by Cdc28p and dephosphorylated by Cdc14p before cytokinesis; high-copy suppressor of synthetic lethality of sis2 sit4 double mutant;		S202			SIT4	32

	VHS2 has a paralog, MLF3, that arose from the whole genome duplication						
			S301	CDC28	CDC28		7, 139, 142, 152, 217, 374, 379
			S				7, 139, 142, 374, 379
			S325			PTP1	32, 142, 152, 217
			S330			PTP1	32, 142, 152
ASG1	Zinc cluster protein proposed to be a transcriptional regulator; regulator involved in the stress response; null mutants have a respiratory deficiency, calcofluor white sensitivity and slightly increased cycloheximide resistance		S166	MEC1, TEL1			7, 52, 370
NUP159	FG-nucleoporin component of central core of the nuclear pore complex; also part of the nuclear pore complex (NPC) cytoplasmic filaments; contributes directly to nucleocytoplasmic transport; regulates ADP release from the ATP-dependent RNA helicase Dbp5p; forms a stable association with Nup82p, Gle2p and two other FG-nucleoporins (Nsp1p and Nup116p)	S402; S404; S940; T948	S182	DUN1			52, 142
			S735	CDC28			7, 116, 122, 142, 217, 373, 379
			S854	CLB2, CDC28			142
HOS4	Subunit of the Set3 complex; complex is a meiotic-specific repressor of sporulation specific genes that contains deacetylase activity; potential Cdc28p substrate		S38	SNF1			32, 142, 370, 379
			S290	CLB2, CDC28			142, 379
			S690	CDC28			7, 32, 122, 142, 152, 217, 370, 374, 379

			T37	SNF1	32, 142, 370
SLM1	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; TORC2 complex substrate and effector; protein abundance increases in response to DNA replication stress; SLM1 has a paralog, SLM2, that arose from the whole genome duplication	S145; S150	S157	PKH3	32, 370
			S158	PKH3	32, 370
			S659	PKH1, PKH2	67
YRB2	Protein of unknown function; involved in nuclear processes of the Ran-GTPase cycle; involved in nuclear protein export; contains Ran Binding Domain and FxFG repeats; interacts with Srm1p, GTP-Gsp1p, Rna1p and Crm1p; relocalizes to the cytosol in response to hypoxia; not essential for viability	T117; T123; T124; S125; T126; S128	S14		7, 116, 142, 370, 373
			T31		7, 32, 139, 142, 370, 374, 379
AIM21	Protein of unknown function; involved in mitochondrial migration along actin filament; may interact with ribosomes; GFP-fusion protein colocalizes with Sac1p to the actin cytoskeleton	S36; T40; T84; S119; T121; T180; S183; S185; S281; T282; S476; S477; T480; T552	S183	PSK2	7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			T180	PSK2	7, 32, 142, 152, 217, 370, 374, 379
BUD6	Actin- and formin-interacting protein; participates in actin cable assembly and organization as a nucleation-promoting factor (NPF) for formins Bni1p and Bnr1p; a triple helical coiled-coil domain in the C-terminal region interacts with Bni1p; involved in	S233	S327	CDC28	7, 12, 32, 116, 142, 217, 370, 373, 374, 379

	polarized cell growth; isolated as bipolar budding mutant; potential Cdc28p substrate				
BNI1	Formin; polarisome component; nucleates the formation of linear actin filaments, involved in cell processes such as budding and mitotic spindle orientation which require the formation of polarized actin cables; recruited to the division site in a Glc7p/Ref2p dependent manner following release of Bnr1p; functionally redundant with BNR1	S327; T328	T143	PRK1	418
			T1274	PRK1	418
			T1946	PRK1	418
MAF1	Highly conserved negative regulator of RNA polymerase III; involved in tRNA processing and stability; inhibits tRNA degradation via rapid tRNA decay (RTD) pathway; binds N-terminal domain of Rpc160p subunit of Pol III to prevent closed-complex formation; regulated by phosphorylation mediated by TORC1, protein kinase A, Sch9p, casein kinase 2; localizes to cytoplasm during vegetative growth and translocates to nucleus and nucleolus under stress conditions		S90	TPK1	7, 32, 142, 203, 267, 374, 379
			S101	TPK1	203, 267, 379
			S159	CKA1, CKA2, CKB1, CKB2	119, 379
			S160	CKA1, CKA2, CKB1, CKB2	119
			S161	CKA1, CKA2, CKB1, CKB2	119
			S162	CKA1, CKA2,	119

				CKB1, CKB2	
			S177	TPK1	32, 56, 142, 152, 203, 267
			S178	TPK1	32, 142, 152, 203, 267, 379
			S179	SCH9	32, 152, 379
			S209	TPK1	142, 203, 217, 267, 374
			S210	TPK1	7, 203, 217, 267
			S388	CKA1, CKA2, CKB1, CKB2	119
VNX1	Calcium/H+ antiporter localized to the endoplasmic reticulum membrane; member of the calcium exchanger (CAX) family; potential Cdc28p substrate	S110; T118; S120; S121	S121	CLB2, CDC28	7, 116, 142, 152, 189, 217, 373, 379
			T118	CLB2, CDC28	142
YFL042C; LAM5	Putative sterol transfer protein; one of six StART-like domain-containing proteins in yeast that may be involved in sterol transfer between intracellular membranes; conserved across eukaryotes; has both GRAM and StART-like (VASt) domains; localizes to membrane contact sites throughout the cell, including nucleus-vacuole junctions and ER-mitochondrial contact sites	T110	S103	CDC28	142, 374, 379
			S149	CDC28	139, 142, 217, 379
			T110	CDC28	7, 142, 152, 217, 379
IES1	Subunit of the INO80 chromatin remodeling complex; relocalizes to the cytosol in response to hypoxia	S504	S36	MEC1, TEL1	7, 52

BLM10	Proteasome activator; binds the core proteasome (CP) and stimulates proteasome-mediated protein degradation by inducing gate opening; required for sequestering CP into proteasome storage granule (PSG) during quiescent phase and for nuclear import of CP in proliferating cells; required for resistance to bleomycin, may be involved in protecting against oxidative damage; similar to mammalian PA200	S11; S29; S34; S35; S36; S62; T64	S11	CDC28		7, 116, 142, 181, 373
			S29	CLB2, CDC28		7, 32, 56, 116, 142, 181, 373, 374, 379
			S56	BUD32		7, 32, 56, 100, 139, 142, 152, 181, 217, 370, 374, 379
YPI1	Regulatory subunit of the type I protein phosphatase (PP1) Glc7p; Glc7p participates in the regulation of a variety of metabolic processes including mitosis and glycogen metabolism; in vitro evidence suggests Ypi1p is an inhibitor of Glc7p while in vivo evidence suggests it is an activator; overproduction causes decreased cellular content of glycogen; partial depletion causes lithium sensitivity, while overproduction confers lithium-tolerance	S133	S131	PSK1	CLA4	7, 32, 37, 56, 116, 139, 142, 217, 370, 373, 374
			S133	PSK1		7, 32, 37, 56, 116, 122, 142, 217, 370, 373, 374, 379
IGD1	Cytoplasmic protein that inhibits Gdb1p glycogen debranching activity; required for normal intracellular accumulation of	S14	S95	TPK3		7, 32, 100, 142, 370

	glycogen; phosphorylated in vivo; expression increases during wine fermentation; protein abundance increases in response to DNA replication stress; IGD1 has a paralog, YOL024W, that arose from the whole genome duplication				
LSB3	Protein containing a C-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization; protein abundance increases in response to DNA replication stress; LSB3 has a paralog, YSC84, that arose from the whole genome duplication	T298; S300; S303; S311; S397; S399; T400; S401; S402	S255	CKA1	32
			S256	CKA1	32
			(blank)(blank)	CKA1	(blank)
CKB1	Beta regulatory subunit of casein kinase 2 (CK2); a Ser/Thr protein kinase with roles in cell growth and proliferation; CK2, comprised of CKA1, CKA2, CKB1 and CKB2, has many substrates including transcription factors and all RNA polymerases	S111	S111	RIO1	7, 32, 152, 370
SUM1	Transcriptional repressor that regulates middle-sporulation genes; required for mitotic repression of middle sporulation-specific genes; also acts as general replication initiation factor; involved in telomere maintenance, chromatin silencing; regulated by pachytene checkpoint	S378	S379	CDC28	7, 142, 152, 228, 370, 379
			S712	MEC1, TEL1	7, 52, 142, 370, 379, 527
			S738	CLB2, CDC28	7, 142, 228, 374, 379
			T306	IME2	3, 271
IDS2	Protein involved in modulation of Ime2p activity during meiosis; appears to act indirectly to promote Ime2p-mediated late	S130; S136	S130	CDC28	7, 122, 142, 374

	meiotic functions; found in growing cells and degraded during sporulation						
CTK3	Gamma subunit of C-terminal domain kinase I; CTDK-I phosphorylates RNA polymerase II subunit Rpo21p to affect transcription and pre-mRNA 3' end processing, and also phosphorylates ribosomal protein Rps2p to increase translational fidelity; protein abundance increases in response to DNA replication stress	T34; T35	T34	CTK1			32, 100, 370, 374
MTC1	Protein of unknown function that may interact with ribosomes; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to COPI-coated vesicles (early Golgi); mtc1 is synthetically lethal with cdc13-1	T330; S336; S337; S339; S340; S342	S273		CKA2	YCH1	7, 32, 139, 142, 217, 379
			S			YCH1	7, 32, 139, 142, 217, 379
ALY2	Alpha arrestin; controls nutrient-mediated intracellular sorting of permease Gap1p; interacts with AP-1 subunit Apl4p; phosphorylated by Npr1p and also by cyclin-CDK complex Pcl7p-Pho85p; promotes endocytosis of plasma membrane proteins; ALY2 has a paralog, ALY1, that arose from the whole genome duplication	S155; S168; S172; S213; S740; S741	S176	CLB2, CDC28			142
			S213	CDC28			7, 32, 122, 142, 152, 374, 379
NET1	Core subunit of the RENT complex; involved in nucleolar silencing and telophase exit; stimulates transcription by RNA polymerase I and regulates nucleolar structure; NET1 has a paralog, TOF2, that arose from the whole genome duplication	S231	S30	CDC5			363
			S31	CDC5			363
			S48	CDC5			236, 363, 379
			S56	CDC5			236

	S60	CDC5		37, 142, 152, 236, 363, 379
	S64	CDC5		152, 236, 363, 379
	S166	CDC28		20, 32, 116, 142, 152, 373, 379
	S169	CDC28		32
	S223	CDC5		363
	S224	CDC5		363
	S228	CDC5	CKA2	7, 37, 139, 142, 152, 236, 363, 374, 379
	S			7, 139, 152, 363, 374, 379
	S231	CDC5		7, 20, 37, 142, 152, 217, 236, 363, 374, 379
	S242	CDC5		152, 236, 363, 379
	S252	CDC28		7, 20, 32, 37, 122, 142, 152, 236, 379
	S259	CDC5		20, 32, 152, 236, 379
	S269	CDC5		152, 236, 379
	S280	CDC5		236
	S295	CDC5	SNF1	139, 142, 152, 363, 379

	S			139, 142, 152, 363, 379
	S301	CDC5		363
	S335	CDC5		363
	S447	CLB2, CDC28		32, 37, 142, 379
	S452	CLB2, CDC28		32, 142
	S830	CDC28		7, 32, 37, 142
	S840	RAD53		7, 37, 56, 370, 379
	S1032	CLB2, CDC28	CDC28	7, 20, 32, 116, 139, 142, 217, 373, 374, 379
	S			7, 20, 32, 116, 139, 142, 217, 373, 374, 379
	S1056	CLB2, CDC28		32, 37, 142, 152, 379
	T16	CDC5		363
	T192	CDC5		236
	T194	CDC5		363
	T195	CDC5		363
	T196	CDC5		363
	T197	CDC5		363
	T288	CDC5		236
	T297	CDC28		142, 152, 363, 379
	T302	CDC5		363
	T676	CLB2, CDC28		20, 32, 56, 142, 152, 217, 374, 379

			T1042	CLB2, CDC28		7, 32, 37, 142, 152, 370, 379
BBC1	Protein possibly involved in assembly of actin patches; interacts with an actin assembly factor Las17p and with the SH3 domains of Type I myosins Myo3p and Myo5p; localized predominantly to cortical actin patches	S77; S78; T81; S83; S103; S158; S620; S621; T624; T810; S815; T818; T820; S822; T824; T835; T894; T895; S902	S103	CDC28	PHO85	7, 32, 56, 116, 139, 142, 217, 370, 373, 374, 379
			S			7, 32, 56, 116, 139, 142, 217, 370, 373, 374, 379
			S631	MKK1		7, 32, 122, 142, 152, 217, 379
			S634	MKK1		7, 32, 142, 152, 217, 379
			S638	MKK1		32, 116, 122, 142, 152, 217, 373, 379
			T636	MKK1		32, 116, 122, 142, 152, 373, 379
PTK2	Serine/threonine protein kinase; involved in regulation of ion transport across plasma membrane; carboxyl terminus is essential for glucose-dependent Pma1p activation via phosphorylation of Pma1p-Ser899; enhances spermine uptake; PTK2 has a paralog, PTK1, that arose from the whole genome duplication	T56; S57; S59; S61; S63; S65; S69; S73; S585; T586; S587; T588; S592; S595; S711; S726; T727; T729; T730; T732; S773; S775; S776	S69	CLB2, CDC28		37, 142, 152, 379
			S711	PTK2	CKA2	7, 32, 37, 139, 142,

					217, 374, 379
			S		7, 32, 37, 139, 142, 217, 374, 379
			S752	PTK2	7, 32, 116, 142, 217, 373, 374, 379
			S755	PTK2	32, 142, 217, 379
			S784	CLB2, CDC28	7, 32, 37, 142, 379
			T727	CDC28	142, 217
			T730	CDC28	7, 37, 116, 142, 217, 373, 379
			T737	CDC28	116, 142, 217, 373, 379
ENT3	Protein containing an N-terminal epsin-like domain; involved in clathrin recruitment and traffic between the Golgi and endosomes; associates with the clathrin adaptor Gga2p	S148	S203	BUD32	7, 32, 142, 152, 217, 379
ASK10	Regulator of the Fps1p glycerol channel; under nonstress conditions, binds to Fps1p to positively regulate glycerol transport; under osmotic stress, multiple phosphorylation by Hog1p causes Ask10p to dissociate from Fps1p; forms homodimers and heterodimerizes with paralog Rgc1p; phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p; associates with RNA polymerase II holoenzyme	S1070	T808	CDC28	7, 32, 37, 142, 152, 379
GYP7	GTPase-activating protein for yeast Rab family members; members include Ypt7p (most effective), Ypt1p, Ypt31p, and Ypt32p (in vitro); involved in vesicle mediated		S265	CDC28	142, 379

	protein trafficking; contains a PH-like domain				
SEC16	COPII vesicle coat protein required for ER transport vesicle budding; essential factor in endoplasmic reticulum exit site (ERES) formation, as well as in COPII-mediated ER-to-Golgi traffic; bound to periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p	S28; S30; T2127; S2128; S2130; T2132	S607	CDC28	7, 116, 122, 142, 370, 373, 379
			S841	CTK1	32, 152, 217, 379
			S1515	CDC28	7, 32, 122, 142, 152, 217, 374, 379
LYS20	Homocitrate synthase isozyme and functions in DNA repair; catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; LYS20 has a paralog, LYS21, that arose from the whole genome duplication	T396	T396	CDC28	7, 32, 56, 116, 122, 142, 152, 217, 370, 373, 374, 379
YGR237C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	S125; S127	S117		32, 142, 152, 379
PSP2	Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of group II intron-splicing defects of a mutation in MRS2 and of a conditional mutation in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing		S340	CDC28	7, 32, 139, 142, 217, 374, 379
INP52	Polyphosphatidylinositol phosphatase; dephosphorylates a number of phosphatidylinositol phosphates (PtdInsPs, PIPs) to PI; involved in endocytosis; hyperosmotic stress causes translocation to actin patches; synaptojanin-like protein with a Sac1 domain; INP52 has a paralog, INP53,	S1081; S1082	S1005	CLB2, CDC28	32, 116, 122, 142, 152, 217, 373, 379

	that arose from the whole genome duplication				
			S1016	CLB2, CDC28	32, 142, 152, 217, 379
SKP1	Evolutionarily conserved kinetochore protein; part of multiple protein complexes, including the SCF ubiquitin ligase complex, the CBF3 complex that binds centromeric DNA, and the RAVE complex that regulates assembly of the V-ATPase; protein abundance increases in response to DNA replication stress	S45; S49	S45	PHO85	32, 142, 152, 379
			S47	PHO85	32, 142, 152, 379
			S49	PTK1	32, 142, 152, 379
			T3	MPS1	37
MCM6	Protein involved in DNA replication; component of the Mcm2-7 hexameric helicase complex that binds chromatin as a part of the pre-replicative complex; forms a subcomplex with Mcm4p and Mcm7p	S2; T9; S12	S78	CDC7	7, 323, 379
MDS3	Putative component of the TOR regulatory pathway; negative regulator of early meiotic gene expression; required, with Pmd1p, for growth under alkaline conditions; has an N-terminal kelch-like domain; MDS3 has a paralog, PMD1, that arose from the whole genome duplication	S668; S669; S671; S693; S781; S918; S919; T920; T923; T1156; S1166; T1168	S693	CDC28	7, 32, 37, 116, 142, 217, 370, 373, 374, 379
			S1387	CLB2, CDC28	142, 379
SDS23	Protein involved in cell separation during budding; one of two S. cerevisiae homologs (Sds23p and Sds24p) of the S. pombe Sds23 protein, which is implicated in APC/cyclosome regulation; SDS23 has a paralog, SDS24, that arose from the whole genome duplication	S61; T66; S398; S399; S400; S402; S404; T405; T409; T410; S430	T405	CDC28	142, 217, 379

YGR054W	Eukaryotic initiation factor eIF2A; associates specifically with both 40S subunits and 80 S ribosomes, and interacts genetically with both eIF5b and eIF4E; homologous to mammalian eIF2A	S473; S560; S561; T563; S564; S567; T568; S572; T581; T586; S587	S560	MCK1	TPK1	7, 32, 139, 142, 370, 374
			S			7, 32, 139, 142, 370, 374
			S561	MCK1		7, 32, 142, 370, 374
			S564	MCK1		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			T563	MCK1		7, 32, 116, 142, 152, 217, 370, 373, 374
			T568	MCK1		7, 32, 142, 379
DAM1	Essential subunit of the Dam1 complex (aka DASH complex); cooperates with Duo1p to connect the DASH complex with the microtubules (MT); couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; Ipl1p target for regulating kinetochore-MT attachments		S20	IPL1		49, 139, 142, 177, 254, 374, 379, 392
			S257	IPL1		49, 142, 177, 254, 374, 379
			S265	IPL1		49, 142, 177, 254, 379
			S292	IPL1		49, 142, 177, 374, 379
YGR130C	Component of the eisosome with unknown function; GFP-fusion protein localizes to the	S44; S249; T254; S257; T277; T278;	S343	TPK3		32, 217, 370, 379

	cytoplasm; specifically phosphorylated in vitro by mammalian diphosphoinositol pentakisphosphate (IP7)	S281; S284; S286; T337; S338; T339; T342				
			S347	YPK1		32, 217, 370, 379
DCP2	Catalytic subunit of Dcp1p-Dcp2p decapping enzyme complex; removes 5' cap structure from mRNAs prior to their degradation; also enters nucleus and positively regulates transcription initiation; nudix hydrolase family member; forms cytoplasmic foci upon DNA replication stress; human homolog DCP2 complements yeast dcp2 thermosensitive mutant	S598; S747; S751	S137	STE20		446
HHO1	Histone H1, linker histone with roles in meiosis and sporulation; decreasing levels early in sporulation may promote meiosis, and increasing levels during sporulation facilitate compaction of spore chromatin; binds to promoters and within genes in mature spores; may be recruited by Ume6p to promoter regions, contributing to transcriptional repression outside of meiosis; suppresses DNA repair involving homologous recombination	S130; S173; S174; S176; S177	S130		SIW14	32, 116, 373
FPK1	Ser/Thr protein kinase; phosphorylates several aminophospholipid translocase family members, regulating phospholipid translocation and membrane asymmetry; phosphorylates and inhibits upstream inhibitory kinase, Ypk1p; localizes to the cytoplasm, early endosome/TGN compartments and thplasma membrane; localizes to the shmoo tip where it has a redundant role in the cellular response to mating pheromone; FPK1 has a paralog, KIN82, that arose from the whole genome duplication	S200; S462; T674; S676	S137	CDC28		7, 32, 142, 152, 379
			S140	CDC28		7, 32, 142, 152, 379

			S144	CDC28	32, 142, 152, 379
			S175	CDC28	7, 142
			S198	CDC28	7, 142
			S339	CDC28	7, 142, 152, 370, 379
			T201	CDC28	142, 217
MDG1	Plasma membrane protein; involved in G-protein mediated pheromone signaling pathway; overproduction suppresses bem1 mutations; MDG1 has a paralog, CRP1, that arose from the whole genome duplication	S160; T164; S178; T180; T181; T182; S227; T256; S257; S263; S272	S288	CKA1	7, 32, 116, 122, 142, 152, 373, 374, 379
			S291	PSK2	7, 32, 116, 122, 142, 373, 374, 379
			T290	PSK2	7, 32, 116, 122, 142, 152, 373, 374
BNI5	Linker protein responsible for recruitment of myosin to the bud neck; interacts with the C-terminal extensions of septins Cdc11p and Shs1p and binds Myo1p to promote cytokinesis	S263; S270; S273; T274; T280	S270	SNF1	7, 32, 100, 139, 142, 217, 280, 370, 374, 379
			S273		7, 32, 100, 142, 217, 280, 281, 370, 379
			T274		7, 32, 100, 142, 280, 370, 379
CBK1	Serine/threonine protein kinase of the the RAM signaling network; Ndr/LATS family member; binds regulatory subunit Mob2p; involved in regulation of cellular morphogenesis, polarized growth, and septum destruction; phosphorylation by Cbk1p regulates localization and activity of Ace2p transcription factor and Ssd1p	S63; S66	S570	CBK1	155, 300

	translational repressor; Cbk1p activity is regulated by both phosphorylation and specific localization; relocalizes to cytoplasm upon DNA replication stress				
			T93	CLB2, CDC28	142
			T109	CLB2, CDC28	7, 142, 379
NSG2	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; NSG2 has a paralog, NSG1, that arose from the whole genome duplication	S49; S81; S82	S90	YPK1	7, 32, 100, 142, 152, 217, 370, 374, 379
			S92	YPK1	32, 142, 217, 370, 379
			S93	YPK1	7, 32, 100, 142, 152, 217, 370, 374, 379
CRZ1	Transcription factor, activates transcription of stress response genes; nuclear localization is positively regulated by calcineurin-mediated dephosphorylation; rapidly localizes to the nucleus under blue light stress; can be activated in stochastic pulses of nuclear localization in response to calcium		S409	TPK1	170
			S410	TPK1	142, 170, 370, 379
			S423	TPK1	32, 56, 170
			S427	TPK1	7, 32, 56, 170, 379
			S429	TPK1	7, 32, 170, 379
SUR7	Plasma membrane protein, component of eisosomes; long-lived protein that remains stable in eisosomes of mother cells while other eisosome proteins, Pil1p and Lsp1p,	T249; T251; S259; S261; S266; S267; T273; S293; S301	S261	TPK3	32, 379

	turn over; may function to anchor the eisosome in place; sporulation and plasma membrane sphingolipid content are altered in mutants; localizes to furrow-like invaginations (MCC patches)				
DAK1	Dihydroxyacetone kinase; required for detoxification of dihydroxyacetone (DHA); involved in stress adaptation		S563	MEC1, TEL1	7, 52
GPD1	NAD-dependent glycerol-3-phosphate dehydrogenase; key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high-osmolarity glycerol response pathway; protein abundance increases in response to DNA replication stress; constitutively inactivated via phosphorylation by the protein kinases Ypk1p and Ypk2p, dephosphorylation increases catalytic activity; forms a heterodimer with Pnc1p to facilitate its peroxisomal import	S23; S24; S25; S27	S24	CTK1	7, 32, 100, 116, 122, 142, 152, 168, 217, 294, 370, 373, 379
			S27	CTK1	7, 32, 100, 116, 122, 142, 152, 168, 217, 294, 370, 373, 374, 379
SLT2	Serine/threonine MAP kinase; coordinates expression of all 19S regulatory particle assembly-chaperones (RACs) to control proteasome abundance; involved in regulating maintenance of cell wall integrity, cell cycle progression, nuclear mRNA retention in heat shock, septum assembly; required for mitophagy, pexophagy; affects recruitment of mitochondria to phagophore assembly site; plays role in adaptive response of cells to cold; regulated by the PKC1-mediated signaling pathway		S423	RAD53	7, 37, 379, 398

			S428	MEC1, TEL1	7, 37, 398
REG1	Regulatory subunit of type 1 protein phosphatase Glc7p; involved in negative regulation of glucose-repressible genes; involved in regulation of the nucleocytoplasmic shuttling of Hxk2p; REG1 has a paralog, REG2, that arose from the whole genome duplication	S254; Y497; S570; S572; S576; T579; S582; S775; T776; S778; Y780; S976; S977; S1013; S1014	S421	CDC28	7, 32, 37, 142, 217, 370, 379
			S898	CDC28	7, 142, 379
			T896	CDC28	142, 379
NPL3	RNA-binding protein; promotes elongation, regulates termination, and carries poly(A) mRNA from nucleus to cytoplasm; represses translation initiation by binding eIF4G; required for pre-mRNA splicing; interacts with E3 ubiquitin ligase Bre1p, linking histone ubiquitination to mRNA processing; may have role in telomere maintenance; dissociation from mRNAs promoted by Mtr10p; phosphorylated by Sky1p in cytoplasm; protein abundance increases in response to DNA replication stress		S224	DUN1	7, 32, 52, 75, 122, 139, 142, 217, 370, 374, 379
			S349	MKK1	32, 75, 100, 379
			S356	RIM11	32, 75
			S411	SKY1	17, 75, 114, 115, 238, 239, 357, 450
RSC4	Component of the RSC chromatin remodeling complex; found in close proximity to nucleosomal DNA; displaced from the surface of nucleosomal DNA after chromatin remodeling; acetylated (K25) by Gcn5p, altering replication stress tolerance; contains tandem bromodomains that recognize histone H3 acetylated on K14 (H3K14ac) by Gcn5p		S545	MEC1, TEL1	7, 52, 379

RPL6A	Ribosomal 60S subunit protein L6A; N-terminally acetylated; binds 5.8S rRNA; homologous to mammalian ribosomal protein L6, no bacterial homolog; RPL6A has a paralog, RPL6B, that arose from the whole genome duplication		S12		SIT4	7, 32, 122, 139, 142, 370, 374, 379
MLP1	Myosin-like protein associated with the nuclear envelope; nuclear basket protein that connects the nuclear pore complex with the nuclear interior; involved with Tel1p in telomere length control; involved with Pml1p and Pml39p in nuclear retention of unspliced mRNAs; MLP1 has a paralog, MLP2, that arose from the whole genome duplication	S333; T337	S1670	DUN1		7, 32, 52
			S1675	CDC28		32, 379
			S1710	RAD53		7, 139, 142, 370, 379
			S1723	DUN1		7, 52
ROD1	Alpha-arrestin involved in ubiquitin-dependent endocytosis; activating dephosphorylation relays glucose signaling to transporter endocytosis; calcineurin dephosphorylation is required for Rsp5p-dependent internalization of agonist-occupied Ste2p, as part of signal desensitization; recruits Rsp5p to Ste2p via its 2 PPXY motifs; protein abundance increases in response to DNA replication stress; ROD1 has a paralog, ROG3, that arose from the whole genome duplication	S602; S720	S447	SNF1		11, 361
MUK1	Guanine nucleotide exchange factor (GEF); involved in vesicle-mediated vacuolar transport, including Golgi-endosome trafficking and sorting through the multivesicular body (MVB); specifically stimulates the intrinsic guanine nucleotide exchange activity of Rab family members (Vps21p/Ypt52p/Ypt53p); partially redundant with GEF VPS9; required for	S67; T71; T498	S67	CDC28		7, 142, 374, 379

	localization of the CORVET complex to endosomes; contains a VPS9 domain					
			S245	CLB2, CDC28		7, 32, 116, 142, 373, 374, 379
SVL3	Protein of unknown function; mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; relocalizes from bud neck to cytoplasm upon DNA replication stress; SVL3 has a paralog, PAM1, that arose from the whole genome duplication	S551	S551	CTK1		7, 32, 122, 142, 152, 217, 370, 374, 379
			T665	PKH3		32
HEH2	Inner nuclear membrane (INM) protein; contains helix-extension-helix (HEH) motif, nuclear localization signal sequence; targeting to the INM requires the Srp1p-Kap95p karyopherins and the Ran cycle; HEH2 has a paralog, SRC1, that arose from the whole genome duplication	S141; S145	S123	CLB2, CDC28		56, 139, 142, 370, 374, 379
PKH3	Protein kinase with similarity to mammalian PDK1 and yeast Pkh1p/Phk2p; yeast Pkh1p and Pkh2p are two redundant upstream activators of Pkc1p; identified as a multicopy suppressor of a pkh1 pkh2 double mutant		S834	PTK2		32, 37, 379
			T832	PTK2		32, 37, 379
STE20	Cdc42p-activated signal transducing kinase; involved in pheromone response, pseudohyphal/invasive growth, vacuole inheritance, down-regulation of sterol uptake; GBB motif binds Ste4p; member of the PAK (p21-activated kinase) family	T203; T207; T216; T408; T411; T413; S418; T546; S547; T552; S924	S206	CDC28		32, 217, 379
			S269		PSR2	32
			S502	CLB2, CDC28		7, 37, 116, 142, 290, 373, 374, 379

			S517	CDC28	32, 37, 56, 142, 370, 379
			S547	CDC28, CLN2	32, 37, 56, 116, 142, 217, 290, 370, 373, 374, 379
			S562	CDC28, CLN2	7, 32, 37, 56, 116, 142, 217, 290, 370, 373, 374, 379
			T203	CLB2, CDC28	7, 32, 142, 217, 370, 379
			T217	CTK1	32, 370, 379
			T218	PKP2	32, 379
			T511	SNF1	32, 370
			T512	CLB2, CDC28	37, 142, 370, 379
			T777	STE20	430
TCB3	Cortical ER protein involved in ER-plasma membrane tethering; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to the plasma membrane (PM) and regulate PM phosphatidylinositol-4-phosphate (PI4P) levels by controlling access of Sac1p phosphatase to its substrate PI4P in the PM; localized to the bud via specific mRNA transport; non-tagged protein detected in a phosphorylated state in mitochondria; C-termini of Tcb1p, Tcb2p and Tcb3p interact	S1335; S1340; S1342; S1346; T1347; T1350; S1354; Y1357; S1360; T1364; Y1366; S1371; S1373; T1379; T1382; S1383; S1386	S1373	CLB2, CDC28	142, 374, 379
			T1350	CDC28	7, 32, 100, 122, 142, 152, 217, 331, 370, 374, 379

TAF12	Subunit (61/68 kDa) of TFIID and SAGA complexes; involved in RNA polymerase II transcription initiation and in chromatin modification, similar to histone H2A; overexpression of the human ortholog, TAF12, an oncogene involved in the formation of choroid plexus carcinomas, results in dosage chromosomal instability (dCIN) in a human cell line similar to the dCIN observed in yeast overexpressors		S325	MEC1, TEL1	7, 52, 379
NUP53	FG-nucleoporin component of central core of nuclear pore complex (NPC); also part of the NPC nuclear basket; contributes directly to nucleocytoplasmic transport; involved in regulation of transcription and mitosis; induces membrane tubulation, which may contribute to nuclear pore assembly; NUP53 has a paralog, ASM4, that arose from the whole genome duplication		S101	CDC28	7, 142, 217, 240, 370, 379
			S206	CDC28	240, 379
GIS1	Histone demethylase and transcription factor; regulates genes during nutrient limitation; activity modulated by proteasome-mediated proteolysis; has JmjC and JmjN domain in N-terminus that interact, promoting stability and proper transcriptional activity; contains two transactivating domains downstream of Jmj domains and a C-terminal DNA binding domain; relocalizes to the cytosol in response to hypoxia; GIS1 has a paralog, RPH1, that arose from the whole genome duplication	S747	S425	CDC28	7, 32, 142, 374
			S696	CDC28	7, 142, 217, 370, 374, 379
CUE4	Protein of unknown function; has a CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; CUE4 has a paralog, CUE1, that arose from the whole genome duplication	T32; S41; S48; S54	S48	KNS1	7, 32, 142, 370, 379

SEG1	Component of eisosome required for proper eisosome assembly; precedes Pil1p/Lsp1p during eisosome formation, controls eisosome length and shape; diffusely distributed, forms heterogeneous patches at plasma membrane in small buds, also found in medium and large buds; expression repressed by cAMP; similar to A. gossypii SEG gene and to S. pombe Sle1p, important for generating eisosomes; SEG1 has a paralog, SEG2, that arose from the whole genome duplication	S302; S318; S450; T452	S658	CLB2, CDC28	7, 142, 379
			S870	CDC28	142
			T675	CLB2, CDC28	7, 32, 56, 142, 370, 374, 379
YMR196W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YMR196W is not an essential gene	T1008; S1010; T1013; S1016; S1020	S1081	CDC28	7, 139, 142, 379
BUD22	Protein required for rRNA maturation and ribosomal subunit biogenesis; required for 18S rRNA maturation; also required for small ribosomal subunit biogenesis; cosediments with pre-ribosomal particles; mutation decreases efficiency of +1 Ty1 frameshifting and transposition, and affects budding pattern	T257; T283; T284; S285	T257	SNF1	7, 32, 56, 116, 139, 142, 217, 370, 373, 374, 379
MYO5	One of two type I myosin motors; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; MYO5 has a paralog, MYO3, that arose from the whole genome duplication	S357; Y359; T1034; T1036; S1038; S1040; S1045; T1048; T1051	S357	YPK2	7, 32, 56, 116, 121, 122, 142, 152, 217, 370, 373, 374, 379
GAL83	One of three possible beta-subunits of the Snf1 kinase complex; allows nuclear localization of the Snf1 kinase complex in the presence of a nonfermentable carbon		S64	SNF1	246

	source; necessary and sufficient for phosphorylation of the Mig2p transcription factor in response to alkaline stress; functionally redundant with SIP1 and SIP2 for the phosphorylation of Mig1p in response to glucose deprivation; contains a glycogen-binding domain						
			S65	SNF1			246
			S87	CKA1, CKA2, CK1B1, CKB2			246
			S93	CKA1, CKA2, CK1B1, CKB2			246
			T90	CKA1, CKA2, CK1B1, CKB2			246
RCO1	Essential component of the Rpd3S histone deacetylase complex; interacts with Eaf3p	S683	S68				7, 52, 139
TRI1	Non-essential sumoylated protein of unknown function; similar to components of human SWI/SNF complex including SMRD3; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, nucleus and nucleolus; TRI1 has a paralog, UAF30, that arose from the whole genome duplication	S113	S113	CDC28	CDC28		7, 139, 142, 379
EIS1	Component of the eisosome required for proper eisosome assembly; similar to Uso1p; authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies; protein increases in abundance and relocalizes from plasma membrane to cytoplasm upon DNA replication stress; EIS1 has a paralog, YKL050C, that arose from the whole genome duplication	T18; S19; S23; S26; S130; S133; S151; S179; S584; S701; Y704; T706; S710; T759; T761; S762; S763; T767; S775; S780; S781; S791; S795; S825; S828; S829; S838	S23			SIW14	32, 56, 116, 142, 370, 373, 379

	S30			SIW14	32
	S130	MCK1	SCH9		7, 32, 56, 116, 139, 142, 152, 331, 373, 374, 379
	S				7, 32, 56, 116, 139, 142, 152, 331, 373, 374, 379
	S133	MCK1			7, 32, 56, 116, 152, 373, 379
	S136	SNF1			32, 116, 152, 373, 379
	S139	SNF1			32, 379
	S584	YPK1	TPK1		7, 32, 56, 116, 122, 139, 142, 217, 370, 373, 374, 379
	S				7, 32, 56, 116, 122, 139, 142, 217, 370, 373, 374, 379
	S762	PSK2		YVH1	32, 370, 374
	S763	PKP1		YVH1	7, 32, 116, 142, 152, 370, 373, 374, 379
	S775	CKA1	HRR25		7, 32, 116, 139, 142, 152, 370, 373, 379

			S				7, 32, 116, 139, 142, 152, 370, 373, 379
			S791	FRK1			32
			T767	PSK2			32, 152, 379
ASM4	FG-nucleoporin component of central core of nuclear pore complex (NPC); contributes directly to nucleocytoplasmic transport; induces membrane tubulation, which may contribute to nuclear pore assembly; ASM4 has a paralog, NUP53, that arose from the whole genome duplication		S464	CDC28			142, 379
MSC3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; msc3 mutants are defective in directing meiotic recombination events to homologous chromatids; potential Cdc28p substrate; protein abundance increases in response to DNA replication stress	S80; S82; S83; T144; S151; S155; Y357; S363; T646; S648; S658; S659; S660	S46	CDC28			142
YLR257W	Protein of unknown function; protein abundance increases in response to DNA replication stress	S66; S129; S135; S137; S139; T142; S143	S197	HOG1	PKC1	PPH21	7, 32, 116, 139, 142, 217, 370, 373, 379
			S200		CKA2	PPH21	7, 32, 56, 116, 139, 370, 373, 379
			S252	PTK1			7, 32, 370, 379
			T8	FRK1			7, 32, 142, 152, 217, 374, 379
FPR4	Peptidyl-prolyl cis-trans isomerase (PPIase); nuclear proline isomerase; affects expression of multiple genes via its role in nucleosome assembly; catalyzes isomerization of proline residues in histones H3 and H4, which affects lysine methylation of those histones;	S80; S82	S80	KIN28	CKA2		7, 32, 37, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379

	PPIase domain acts as a transcriptional repressor when tethered to DNA by lexA, and repressor activity is dependent on PPIase activity; contains a nucleoplasmin-like fold and can form pentamers						
			S82	KIN28	CKA2		7, 32, 37, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
SKG3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate; similar to Skg4p; relocalizes from bud neck to cytoplasm upon DNA replication stress; SKG3 has a paralog, CAF120, that arose from the whole genome duplication	S633	S633	SNF1			32, 56, 116, 217, 373, 379
MMR1	Phosphorylated protein of the mitochondrial outer membrane; localizes only to mitochondria of the bud; interacts with Myo2p to mediate mitochondrial distribution to buds; mRNA is targeted to the bud via the transport system involving She2p		S37	CDC28			32, 122, 142, 379
BCP1	Essential protein involved in nuclear export of Mss4p; Mss4p is a lipid kinase that generates phosphatidylinositol 4,5-biphosphate and plays a role in actin cytoskeleton organization and vesicular transport	T205	T205		CKA2	SIT4	7, 32, 116, 139, 142, 152, 217, 370, 373, 374
ESF1	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels	S86; S372	S86	FUS3			7, 32, 116, 139, 142, 152, 217, 373, 374, 379
			S223			CMP2	7, 32, 116, 139, 142, 217, 373, 374, 379

			T220			CMP2	32, 56, 116, 139, 373, 379
VPS74	Golgi phosphatidylinositol-4-kinase effector and PtdIns4P sensor; interacts with the cytosolic domains of cis and medial glycosyltransferases, and in the PtdIns4P-bound state mediates the targeting of these enzymes to the Golgi; interacts with the catalytic domain of Sac1p, the major cellular PtdIns4P phosphatase, to direct dephosphosphorylation of the Golgi pool of PtdIns4P; tetramerization required for function; ortholog of human GOLPH3/GPP34/GMx33	S14; T17; S18; S19; S22; S23	S14	SNF1	RIM11		7, 32, 56, 100, 139, 142, 144, 370, 374, 379
			S19	PTK2			7, 32, 56, 100, 144, 370, 379, 402
			S23	PTK2			32, 100, 144, 370, 379
CRN1	Coronin; cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; plays a role in regulation of actin patch assembly	S456; S460; S462; S463; S465; S484; S485; T520; T565; S567; S573; T575; S578; S579; T600; S601	S463			PPH21	7, 32, 56, 116, 142, 217, 370, 373, 374, 379
SPN1	Protein involved in RNA polymerase II transcription; is constitutively recruited to the CYC1 promoter and is required for recruitment of chromatin remodeling factors for the expression of CYC1 gene; interacts genetically or physically with RNAP II, TBP, TFIIS, and chromatin remodelling factors; central domain highly conserved throughout eukaryotes; mutations confer an Spt- phenotype	T15; S85; T86; S89; T120	S23	MEC1, TEL1			7, 32, 52, 116, 142, 152, 217, 370, 373, 374, 379
			S89	SSK2			7, 32, 56, 116, 142,

					192, 217, 370, 373, 374, 379
			S118	KNS1	32, 370, 379
ATG13	Regulatory subunit of the Atg1p signaling complex; stimulates Atg1p kinase activity; required for vesicle formation during autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; contains a HORMA domain required for autophagy and for recruitment of the phosphatidylinositol 3-kinase complex subunit Atg14p to the pre-autophagosomal structure		S344	TPK1	142, 377
			S346	TPK1	142, 152, 374, 377, 379
			S348	TOR1	7, 142, 152, 173, 174, 374, 379
			S437	TOR1	32, 37, 152, 173, 174, 377
			S438	TOR1	32, 152, 173, 174
			S496	TOR1	152, 173, 174
			S535	TOR1	142, 152, 173, 174
			S541	TOR1	7, 142, 152, 173
			S581	TPK1	377
			S646	TOR1	142, 152, 173, 174, 379
			S649	TOR1	7, 122, 142, 152, 173, 174, 374, 379
VIP1	Inositol hexakisphosphate and inositol heptakisphosphate kinase; inositol	T143; S145	S141	MKK2	7, 32, 116, 142, 217,

	heptakisphosphate (IP7) production is important for phosphate signaling; involved in cortical actin cytoskeleton function, and invasive pseudohyphal growth analogous to S. pombe asp1; inositol hexakisphosphate is also known as IP6				370, 373, 374, 379
			S1107	CDC28	7, 32, 37, 116, 122, 142, 373, 374, 379
			S1121	PTK1	32
NVJ2	Lipid-binding ER protein, enriched at nucleus-vacuolar junctions (NVJ); may be involved in sterol metabolism or signaling at the NVJ; contains a synaptotagmin-like-mitochondrial-lipid binding protein (SMP) domain; binds phosphatidylinositols and other lipids in a large-scale study; may interact with ribosomes, based on co-purification experiments	S591; S621; S622; T624; S640; S646	S676	CDC28	7, 122, 142, 217, 370, 379
SSK1	Cytoplasmic phosphorelay intermediate osmosensor and regulator; part of a two-component signal transducer that mediates osmosensing via a phosphorelay mechanism; required for mitophagy; dephosphorylated form is degraded by the ubiquitin-proteasome system; potential Cdc28p substrate		S195	CDC28	7, 32, 142, 379
			S673	CDC28	32, 56, 116, 142, 217, 373, 379
HBT1	Shmoo tip protein, substrate of Hub1p ubiquitin-like protein; mutants are defective for mating projection formation, thereby implicating Hbt1p in polarized cell morphogenesis; HBT1 has a paralog, YNL195C, that arose from the whole genome duplication	Y29; S41; S43; T45; S251; T259; S301; S303; Y362; S363; S427; Y428; S431; S795; S843; S850; Y855; S856; S857; S932; T939; T940; S941; Y942; S943; T948; T949; S950; S956; S959;	S41	SAT4	7, 32, 116, 142, 373

S962; S983; S990; T991; S993; Y1003; S1005; S1036					
	S43	PBS2			32, 116, 142, 373
	S251			SIW14	32
	S257			SIW14	32
	S301	PSK2			32, 142
	S303	MCK1			32, 142, 370, 374
	S363	PKP1		PPH22	7, 32, 56, 116, 142, 370, 373
	S561			PPH22	32, 142
	S671	CDC28		PPS1	32, 142
	S856	PKP1			32, 142
	S857	MCK1		PPH22	32, 142, 374
	S956	MCK1			7, 32, 100, 116, 142, 370, 373, 374
	S959	MCK1		PPH22	32, 100, 116, 142, 373, 374
	S962	PKP1		PPH22	32, 100, 116, 142, 373, 374
	S990	CMK1			32
	S1034	PKP1	CLA4		7, 32, 116, 122, 139, 142, 217, 373
	S				7, 32, 116, 122, 139, 142, 217, 373

			S1036	CLA4		PPH22	7, 32, 116, 122, 142, 373
			T366	PSK2			7, 32, 370
			T368	PKP1			32
			T949	PBS2			32
			T991	PKP1			32
			T997	MCK1			32, 56, 100, 142
			Y362	PBS2			32
			Y987	MCK1			32
VPS13	Protein involved in prospore membrane morphogenesis; peripheral membrane protein that localizes to the prospore membrane and at numerous membrane contact sites; involved in sporulation, vacuolar protein sorting, prospore membrane formation during sporulation, and protein-Golgi retention; required for mitochondrial integrity; contains a PH-like domain; homologous to human CHAC and COH1 which are involved in Chorea-acanthocytosis and Cohen syndrome, respectively	T433; S436; T438; T440	S1715	RCK2	PKC1		7, 32, 122, 139, 142, 217, 370, 379
			S				7, 32, 122, 139, 142, 217, 370, 379
			T1379	CDC28	CDC28		7, 32, 100, 139, 142, 379
			T				7, 32, 100, 139, 142, 379
ZEO1	Peripheral membrane protein of the plasma membrane; interacts with Mid2p; regulates the cell integrity pathway mediated by Pkc1p and Slt2p; the authentic protein is detected in a phosphorylated state in highly purified mitochondria	S40; T49	S85	BUD32			32, 116, 152, 373

			S89	PTK1		32, 116, 152, 373, 379
			T49	VPS34	CDC28	7, 32, 56, 116, 122, 139, 142, 152, 217, 331, 370, 373, 379
			T			7, 32, 56, 116, 122, 139, 142, 217, 331, 370, 373, 379
RTC1	Subunit of SEACAT, a subcomplex of the SEA complex; Rtc1p, along with Mtc5p and Sea4p, redundantly inhibit the TORC1 inhibitory role of the Iml1p/SEACIT (Iml1p-Npr2p-Npr3p) subcomplex, a GAP for GTPase Gtr1p (EGOC subunit) in response to amino acid limitation, thereby resulting in activation of TORC1 signaling; SEA is a coatomer-related complex that associates dynamically with the vacuole; has N-terminal WD-40 repeats and a C-terminal RING motif; null suppresses cdc13-1		S946	SNF1		7, 32, 142, 370, 379
			S950	SNF1		7, 32, 116, 142, 217, 370, 373, 379
CUE5	Ubiquitin-binding protein; functions as ubiquitin-Atg8p adaptor in ubiquitin-dependent autophagy; serves as proteaphagy receptor for inactivated 26S proteasomes; contains CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; CUE5 has a paralog, DON1, that arose from the whole genome duplication; human TOLLIP is a functional	S21; S36; S45; T50; T70; S220; T346; S348; S351; T352	S21	MKK1		7, 32, 116, 142, 217, 370, 373, 379

	CUE-domain homolog, can complement yeast null mutant, rescuing hypersensitivity of cue5 null mutant cells to Htt-96Q				
			S220	KSP1	7, 32, 142, 217, 374, 379
			T364	CLB2, CDC28	7, 32, 100, 116, 142, 152, 217, 370, 373, 379
			T367	CDC28	32, 100, 142, 152, 370, 379
			T369	CDC28	7, 32, 152
ETT1	Nuclear protein that inhibits replication of Brome mosaic virus; S. cerevisiae is a model system for studying replication of positive-strand RNA viruses in their natural hosts; deletion increases stop codon readthrough	S30; S33	T34	SNF1	7, 32, 142, 152, 370, 374, 379
VHS3	Negative regulatory subunit of protein phosphatase 1 Ppz1p; involved in coenzyme A biosynthesis; subunit of the phosphopantothenoylcysteine decarboxylase (PPCDC; Cab3p, Sis2p, Vhs3p) complex and the CoA-Synthesizing Protein Complex (CoA-SPC: Cab2p, Cab3p, Cab4p, Cab5p, Sis2p and Vhs3p)	T108; T183; S221; S223; T224; S225	S223	RTK1	7, 32, 142, 217
			S225	CDC28	7, 32, 142, 374
SGT1	Cochaperone protein; regulates activity of adenylyl cyclase Cyr1p; involved in kinetochore complex assembly; associates with the SCF (Skp1p/Cdc53p/F box protein) ubiquitin ligase complex; acts as a linker between Skp1p and HSP90 complexes; protein abundance increases in response to DNA replication stress	S165; S166; S168	S171	CDC28	7, 116, 142, 217, 373, 374, 379
			S361	CKA1, CKA2,	22

				CKB1, CKB2	
GYP1	Cis-golgi GTPase-activating protein (GAP) for yeast Rabs; the Rab family members are Ypt1p (in vivo) and for Ypt1p, Sec4p, Ypt7p, and Ypt51p (in vitro); involved in vesicle docking and fusion	S87; S89	S546		7, 142, 379
			T539		7, 142, 379
			T555		142, 379
ALE1	Broad-specificity lysophospholipid acyltransferase; part of MBOAT family of membrane-bound O-acyltransferases; key component of Lands cycle; may have role in fatty acid exchange at sn-2 position of mature glycerophospholipids	S513	S513	PHO85	7, 32, 116, 122, 142, 152, 217, 373, 374, 379
HRK1	Protein kinase; implicated in activation of the plasma membrane H(+)-ATPase Pma1p in response to glucose metabolism; plays a role in ion homeostasis; protein abundance increases in response to DNA replication stress		S47	HRK1	7, 32, 152, 370
TCO89	Subunit of TORC1 (Tor1p or Tor2p-Kog1p-Lst8p-Tco89p); regulates global H3K56ac; TORC1 complex regulates growth in response to nutrient availability; cooperates with Ssd1p in the maintenance of cellular integrity; deletion strains are hypersensitive to rapamycin	S119; S546	S497	PTK2	32, 142, 379
			S500	PTK2	32, 142, 379
			S546	CLB2, CDC28	116, 142, 217, 373, 379
SLF1	RNA binding protein that associates with polysomes; may be involved in regulating mRNA translation; involved in the copper-dependent mineralization of copper sulfide complexes on cell surface in cells cultured in copper salts; SLF1 has a paralog, SRO9, that arose from the whole genome duplication;	S40; S41; S42	S42	CDC28	7, 32, 122, 142, 374, 379

	protein abundance increases in response to DNA replication stress					
RCN2	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; phosphorylated in response to alpha factor; protein abundance increases in response to DNA replication stress	S102; S104; T105; S110; S129; T132; S149; S150; S152; S156; S157; S160; S183; S185; S186; S187; S188; T189; T200; S201; S204; T248; S250; S255; S257; T259	S143	SLT2		32
			S150	SLT2	RIM11	7, 32, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S			7, 32, 139, 217, 379
			S152	TPK2		7, 32, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S157	TPK2		7, 32, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S160	SLT2		7, 32, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			T132	TPK2		7, 32, 142, 217, 370

IOC2	Subunit of the Isw1b complex; exhibits nucleosome-stimulated ATPase activity and acts within coding regions to coordinate transcription elongation with termination and processing; contains a PHD finger motif; other complex members are Isw1p and Ioc4p		S262	MEC1, TEL1			7, 52, 142, 379
			S605	MEC1, TEL1			52
			S760	MEC1, TEL1			52
CHS5	Component of the exomer complex; the exomer which also contains Csh6p, Bch1p, Bch2p, and Bud7, is involved in the export of select proteins, such as chitin synthase Chs3p, from the Golgi to the plasma membrane; interacts selectively with the activated, GTP-bound form of Arf1p; Chs5p is the only protein with a BRCT domain that is not localized to the nucleus	S312; S318; S321; S338; S347; T348; S365; T373; S384; S399; S400; S579; S590; S600	S347			SIT4	32, 370
			T334			SIT4	32, 142, 370, 379
MRH1	Protein that localizes primarily to the plasma membrane; also found at the nuclear envelope; long-lived protein that is asymmetrically retained in the plasma membrane of mother cells; the authentic, non-tagged protein is detected in mitochondria in a phosphorylated state; null mutation confers sensitivity to acetic acid	S289; T295; S299	S289	YPK1	CDC28	SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
			S			SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
			T295	PSK2	CDC28	SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152,

						217, 331, 370, 373, 374, 379
			T		SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
LYS21	Homocitrate synthase isozyme; catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; LYS21 has a paralog, LYS20, that arose from the whole genome duplication	S409; T410	T410	CDC28		7, 32, 56, 116, 142, 217, 370, 373, 374
DCS2	m(7)GpppX pyrophosphatase regulator; non-essential, stress induced regulatory protein; modulates m7G-oligoribonucleotide metabolism; inhibits Dcs1p; regulated by Msn2p, Msn4p, and the Ras-cAMP-cAPK signaling pathway; mutant has increased aneuploidy tolerance; DCS2 has a paralog, DCS1, that arose from the whole genome duplication	S58; S60; S63; T64; T340; S341	S63	PKH2		7, 32, 142, 370, 374
			T64	MCK1		7, 32, 116, 142, 370, 373, 374
MED2	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation; relocalizes to the cytosol in response to hypoxia	T171; T172	S208	SSN3		128, 410
MSL5	Component of commitment complex; which defines first step in splicing pathway; essential protein that interacts with Mud2p and Prp40p, forming a bridge between the intron ends; also involved in nuclear	S93; S95; S376; S378	S376	CDC28		7, 32, 142, 152, 370, 379

	retention of pre-mRNA; relocalizes to the cytosol in response to hypoxia					
			S378	CDC28		7, 32, 142, 152, 370, 379
BUG1	Cis-golgi localized protein involved in ER to Golgi transport; forms a complex with the mammalian GRASP65 homolog, Grh1p; mutants are compromised for the fusion of ER-derived vesicles with Golgi membranes	S2; S87; T275; T277	S87	CKA2		7, 32, 116, 139, 142, 217, 370, 373, 374, 379
			T277	CDC28		142, 379
INP53	Polyphosphatidylinositol phosphatase; dephosphorylates multiple phosphatidylinositol phosphates; involved in trans Golgi network-to-early endosome pathway; hyperosmotic stress causes translocation to actin patches; contains Sac1 and 5-ptase domains; INP53 has a paralog, INP52, that arose from the whole genome duplication	S986; T988	S986	CDC28	PHO85	7, 32, 37, 116, 139, 142, 370, 373, 374, 379
			S			7, 32, 37, 116, 139, 142, 370, 373, 374, 379
			T988	CLB2, CDC28		7, 32, 142, 374
HER1	Protein of unknown function; required for proliferation or remodeling of the ER that is caused by overexpression of Hmg2p; may interact with ribosomes, based on co-purification experiments; HER1 has a paralog, GIP3, that arose from the whole genome duplication	S277; S280; S1013; S1204	S61	CDC28		142, 379
			T128	SNF1		32, 56, 142, 379
MAM3	Protein required for normal mitochondrial morphology; has similarity to hemolysins	S434; S435; S439; S475; T477; T485; T575; T599	S522	MCK1		32, 142
			S523	MCK1		32, 56, 142

			S527	MCK1			32, 56, 116, 142, 373, 379
			T519	MCK1			32, 56, 142, 379
HSP42	Small heat shock protein (sHSP) with chaperone activity; forms barrel-shaped oligomers that suppress unfolded protein aggregation; involved in cytoskeleton reorganization after heat shock; protein abundance increases and forms cytoplasmic foci in response to DNA replication stress	S182; S213; S214; S215; S223; S232; T236	S213	PBS2	TPK1		7, 32, 139, 142, 152, 217, 370, 379
			S				7, 32, 139, 142, 217, 370, 379
			S214	PBS2	SNF1	PPH21	7, 32, 116, 122, 139, 142, 152, 217, 370, 373, 379
			S			PPH21	7, 32, 139, 142, 152, 217, 370, 379
			S215			PPH21	7, 32, 116, 122, 142, 152, 217, 370, 373, 379
			S223			PPH21	7, 32, 142, 379
WHI5	Repressor of G1 transcription; binds to SCB binding factor (SBF) at SCB target promoters in early G1; dilution of Whi5p concentration during cell growth determines cell size; phosphorylation of Whi5p by the CDK, Cln3p/Cdc28p relieves repression and promoter binding by Whi5, and contributes to both the determination of critical cell size	T284; S288	S59				7, 32, 68, 116, 122, 142, 152, 370, 373, 379, 416

	at START and cell fate; periodically expressed in G1					
			S62			7, 32, 68, 116, 122, 142, 152, 370, 373, 379, 416
			S88			142, 152, 416
			S154			7, 32, 68, 142, 152, 379, 384, 416
			S156			7, 32, 68, 142, 152, 370, 379, 384, 416
			S161			7, 32, 68, 142, 152, 370, 379, 384, 416
			T5			68, 189, 416
			T57	CDC28		32, 68, 139, 142, 152, 370, 379, 416
STB3	Ribosomal RNA processing element (RRPE)-binding protein; involved in the glucose-induced transition from quiescence to growth; restricted to nucleus in quiescent cells, released into cytoplasm after glucose repletion; binds Sin3p; relative distribution to the nucleus increases upon DNA replication stress	S9; S307	S337		PTC7	32, 142, 152, 374, 379
			S341		PTC7	32, 56, 152, 379
POM34	Subunit of the transmembrane ring of the nuclear pore complex (NPC); contributes to nucleocytoplasmic transport, NPC biogenesis and spindle pole body duplication		T221	CLB2, CDC28		142, 379

		T273	CDC28			142, 217, 379
PAR32	Protein of unknown function; hyperphosphorylated upon rapamycin treatment in a Tap42p-dependent manner; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; PAR32 is not an essential gene	S36	PHO85	SNF1		7, 32, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
		S				7, 32, 116, 139, 142, 152, 217, 373, 374, 379
		S39	PHO85			7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
		S49	PHO85			32, 152
		S131	VPS15			32
		S138			YCH1	32, 142, 152, 217, 374, 379
		S141			YCH1	32, 37, 142, 152, 217, 370, 379
		S148	CLB2, CDC28			7, 32, 142, 152
		S246	CLB2, CDC28	CDC28		7, 32, 116, 122, 139, 142, 152, 217, 373, 374, 379
		S				7, 32, 116, 122, 139, 142, 152, 217, 373, 374, 379

ENT1	Epsin-like protein involved in endocytosis and actin patch assembly; functionally redundant with Ent2p; binds clathrin via a clathrin-binding domain motif at C-terminus; relocalizes from bud neck to cytoplasm upon DNA replication stress; ENT1 has a paralog, ENT2, that arose from the whole genome duplication	T160; S163	T346	PRK1			7, 56, 116, 146, 370, 373, 374, 379
			T366	PRK1			7, 32, 142, 146, 152, 217, 370, 379
			T395	PRK1			7, 32, 122, 142, 146, 152, 217, 370, 379, 421
			T415	PRK1			146, 421
			T427	PRK1			142, 146
TIF6	Constituent of 66S pre-ribosomal particles; has similarity to human translation initiation factor 6 (eIF6); may be involved in the biogenesis and or stability of 60S ribosomal subunits	S231; S233	S174	HRR25			28, 327
			S175	HRR25			28, 327
HRP1	Subunit of cleavage factor I; cleavage factor I is a five-subunit complex required for the cleavage and polyadenylation of pre-mRNA 3' ends; RRM-containing heteronuclear RNA binding protein and hnRNPA/B family member that binds to poly (A) signal sequences; required for genome stability	S2; S87	S462	CDC28			7, 32, 116, 122, 142, 373, 379
IGO2	Protein required for initiation of G0 program; prevents degradation of nutrient-regulated mRNAs via the 5'-3' mRNA decay pathway; phosphorylated by Rim15p; GFP protein localizes to the cytoplasm and nucleus; IGO2 has a paralog, IGO1, that arose from the whole genome duplication		S119		CLA4	PPH22	32, 139, 142, 379

	S122		PPH22	32, 142, 152, 370, 379
	S128	CLB2, CDC28		32, 142, 152, 370, 379

Table 3.5 Phosphorylated proteins and their kinases and phosphatases in high and low density cells treated with LCA at day 2.

Gene Symbol	Description	PhosphoSite in Sample	PhosphoSite in Literature	Known Kinase	Predicted Kinase	Known Phosphatases	Reference
HXK2	Hexokinase isoenzyme 2; phosphorylates glucose in cytosol; predominant hexokinase during growth on glucose; represses expression of HXK1, GLK1, induces expression of its own gene; antiapoptotic; phosphorylation/dephosphorylation at Ser14 by kinase Snf1p, phosphatase Glc7p-Reg1p regulates nucleocytoplasmic shuttling of Hxk2p; functions downstream of Sit4p in control of cell cycle, mitochondrial function, oxidative stress resistance, chronological lifespan; has paralog HXK1	S15; S158	S15	TPK1	TPK1	GLC7, REG1	7, 10, 11, 29, 32, 100, 122, 138, 139, 142, 152, 179, 190, 324, 374
HTA1	Histone H2A; core histone protein required for chromatin assembly and chromosome function; one of two nearly identical subtypes (see also HTA2); DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p; N-terminally propionylated in vivo	S129	S129	MEC1			52, 85, 100, 116, 134, 183, 379, 404, 409, 435
NOT3	Component of the CCR4-NOT core complex, involved in mRNA decapping; involved in transcription initiation and elongation and in mRNA degradation; conserved lysine in human homolog of Not3p and Not5p is mutated in cancers	S304; S316; T319; S324; S325; S326; S344; S347; S348; S441; S442; S446; S450; T454; S798	S450	PHO85	RIM11		7, 32, 100, 116, 139, 142, 152, 217, 373, 374, 379
			T454	PHO85			7, 32, 100, 116, 142, 152, 217, 373, 374, 379
BCY1	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA); PKA is a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation	S68; S70; S74; S77; S79; T129; S130; T131; T144; S145; S147; T150	S70	MCK1			7, 32, 37, 142, 152, 370, 374, 379

			S89	CDC28		142
			S130	KNS1		7, 32, 142, 217, 370, 374
			S147	KIN4		32, 142, 374
			T129	KNS1		7, 32, 142, 217, 370, 374, 379
			T131	KNS1		7, 32, 37, 56, 142, 217, 370, 374, 379
			T144		CNA1	7, 32, 37, 40, 56, 142, 217, 374
FBP1	Fructose-1,6-bisphosphatase; key regulatory enzyme in the gluconeogenesis pathway, required for glucose metabolism; undergoes either proteasome-mediated or autophagy-mediated degradation depending on growth conditions; glucose starvation results in redistribution to the periplasm; interacts with Vid30p	S12; T13; T18	S12	TPK1		32, 126, 142, 247, 332, 333
CAF20	Phosphoprotein of the mRNA cap-binding complex; involved in translational control; repressor of cap-dependent translation initiation; competes with eIF4G for binding to eIF4E	S91; T99; T101; T102; T104; S105; T106; T111	S58	PSK2		342
			S59	PSK2		342
			S78	FRK1		7, 32, 116, 139, 142, 152, 217, 370, 373, 374, 379
			S91	SLT2	CKA2	7, 32, 116, 139, 142, 217, 370, 373, 374, 379, 452

			T102	SLT2	7, 32, 116, 122, 142, 217, 370, 373, 374, 379
CYC8	General transcriptional co-repressor; acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters; can form the prion [OCT+]	S421; T426; S429; S741; S768; S815; S817; S943	S780	MEC1, TEL1	7, 370
			S815	KNS1	7, 32, 142, 217, 370, 374, 379
			S819	KNS1	32, 142, 379
ABP1	Actin-binding protein of the cortical actin cytoskeleton; important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; inhibits barbed-end actin filament elongation; phosphorylation within its Proline-Rich Regio, mediated by Cdc28p and Pho85p, protects Abp1p from proteolysis mediated by its own PEST sequences; mammalian homolog of HIP-55 (hematopoietic progenitor kinase 1 [HPK1]-interacting protein of 55 kDa)	T157; S163; T165; S167; S169; S174; T181; S183; S313; S475; S478; S481	S26	PTK2	32
			S169	CDC28, CLB2	7, 32, 56, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S183	CDC28	7, 32, 56, 100, 116, 142, 152, 217, 370, 373, 374, 379
			S313	CDC28	7, 32, 116, 142, 373, 379

			T30	PTK2		32
			T31	PTK2		32
			T165	CDC28, CLB2	PHO85	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			T181	CDC28, CLB2	PHO85	7, 32, 56, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
HSP26	Small heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation; long-lived protein that is preferentially retained in mother cells and forms cytoplasmic foci; oligomer activation requires heat-induced conformational change; also has mRNA binding activity	S2; S5; T42; S47; T48; S208; S211	S208	MEC1, TEL1		7, 52, 100, 142, 152, 379
			S211	MEC1, TEL1		7, 52, 100, 122, 139, 142, 152, 374, 379
VMA2	Subunit B of V1 peripheral membrane domain of vacuolar H+-ATPase; electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the cytoplasm; protein abundance increases in response to DNA replication stress; human homolog ATP6V1B1, implicated in autosomal-recessive distal renal tubular acidosis (RTA) with sensorineural deafness, complements yeast null mutant	T501; S503; S504; S511; S515	S503	SNF1		7, 32, 56, 370, 374
			S511	MEC1, TEL1	CKA2	7, 116, 139, 142, 152, 217, 370,

							373, 374, 379
PDA1	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex; catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA; phosphorylated; regulated by glucose; PDH complex is concentrated in spots within the mitochondrial matrix, often near the ERMES complex and near peroxisomes	Y309; S313; S315	S313	PKP1, PKP2	CKA2		7, 32, 56, 100, 110, 122, 139, 142, 152, 217, 258, 331, 370, 374, 379
OM45	Mitochondrial outer membrane protein of unknown function; major constituent of the outer membrane, extending into the intermembrane space; interacts with porin (Por1p) and with Om14p; imported via the presequence pathway involving the TOM and TIM23 complexes, then assembled in the outer membrane by Mim1p; protein abundance increases in response to DNA replication stress	T207	T207		SNF1	PPH22	7, 32, 139, 379
PFK2	Beta subunit of heterooctameric phosphofructokinase; involved in glycolysis; indispensable for anaerobic growth; activated by fructose-2,6-bisphosphate and AMP; mutation inhibits glucose induction of cell cycle-related genes	S36; S41; S42; S47; T48; S148; T149; T152; S160; S163; S166; S167; S171; Y172; T173; Y177	S166	SNF1			7, 32, 116, 142, 152, 217, 370, 373, 379
			S167	SNF1			7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S171	SNF1	CKA2		7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379

			S652	PKC1		7, 81
			Y172	SNF1		7, 32, 56, 116, 139, 142, 217, 370, 373
CBF1	Basic helix-loop-helix (bHLH) protein; forms homodimer to bind E-box consensus sequence CACGTG present at MET gene promoters and centromere DNA element I (CDEI); affects nucleosome positioning at this motif; associates with other transcription factors such as Met4p and Isw1p to mediate transcriptional activation or repression; associates with kinetochore proteins, required for chromosome segregation; protein abundance increases in response to DNA replication stress	T138; S140; S149	S45	MEC1, TEL1		7, 32, 52, 116, 142, 152, 370, 373, 379
			S48	MEC1, TEL1		7, 32, 52, 116, 142, 152, 370, 373, 379
			S155	SSN3		7, 32, 142, 217, 370, 379
			S156	SSN3		7, 32, 142, 217, 370, 379
			T138	SSN3	CDC28	7, 32, 139, 142, 217, 379
			T154	CTK1		7, 32, 116, 142, 370, 373, 379
SUI2	Alpha subunit of the translation initiation factor eIF2; eIF2 is involved in identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; protein abundance increases in response to DNA replication stress	S292; S294; S301	S52	GCN2		76, 374, 387, 411, 459

			S292	CKA1, CKA2, CKB1, CKB2		7, 98, 100, 116, 142, 152, 373, 374, 379, 411
			S294	CKA1, CKA2, CKB1, CKB2		7, 98, 100, 116, 142, 152, 373, 374, 379, 411
			S301	CKA1, CKA2, CKB1, CKB2		7, 98, 100, 116, 142, 152, 373, 374, 379, 411
MCK1	Dual-specificity ser/thr and tyrosine protein kinase; roles in chromosome segregation, meiotic entry, genome stability, phosphorylation-dependent protein degradation (Rcn1p and Cdc6p), inhibition of protein kinase A, transcriptional regulation, inhibition of RNA pol III, calcium stress and inhibition of Clb2p-Cdc28p after nuclear division; MCK1 has a paralog, YGK3, that arose from the whole genome duplication	S24; S27; T30; S196; S198; Y199; S202	Y199	MCK1		7, 32, 142, 152, 217, 328, 374, 379
GSY1	Glycogen synthase; expression induced by glucose limitation, nitrogen starvation, environmental stress, and entry into stationary phase; GSY1 has a paralog, GSY2, that arose from the whole genome duplication; relocalizes from nucleus to cytoplasmic foci upon DNA replication stress	S651; S655	S651	MCK1	RIM11	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S655	MCK1	PHO85	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379

MBR1	Protein involved in mitochondrial functions and stress response; overexpression suppresses growth defects of hap2, hap3, and hap4 mutants; MBR1 has a paralog, ISF1, that arose from the whole genome duplication	S222; S224; S226; S227	S69			142
NAP1	Histone chaperone; involved in histone exchange by removing and replacing histone H2A-H2B dimers or histone variant dimers from assembled nucleosomes; involved in the transport of H2A and H2B histones to the nucleus; required for the regulation of microtubule dynamics during mitosis; interacts with mitotic cyclin Clb2p; controls bud morphogenesis; phosphorylated by CK2; protein abundance increases in response to DNA replication stress	T20; T24	S159	CKA1, CKA2, CKB1, CKB2		7, 32, 37, 43, 116, 139, 142, 152, 217, 370, 373
			S177	CKA1, CKA2, CKB1, CKB2	CKA2	7, 32, 37, 43, 116, 139, 142, 152, 217, 370, 373, 379
			S397	CKA1, CKA2, CKB1, CKB2		7, 43
			T20	PTK2		7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
			T24	PTK2		7, 32, 37, 116, 122, 142, 152, 217, 373, 374, 379
FEN1; ELO2	Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory	T334; S336; S338	S336	MCK1	PHO85	7, 32, 56, 100, 139, 142, 152,

	effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; ELO2 has a paralog, ELO1, that arose from the whole genome duplication; lethality of the elo2 elo3 double null mutation is functionally complemented by human ELOVL1 and weakly complemented by human ELOVL3 or ELOV7					217, 370, 374, 379
			S338	MCK1		7, 32, 56, 100, 142, 152, 217, 370, 374, 379
			T334	MCK1	PHO85	7, 32, 56, 100, 139, 142, 152, 217, 370, 374, 379
RPC53	RNA polymerase III subunit C53	S119; S224; T228; T232; S234	S224	MCK1		7, 32, 56, 116, 142, 152, 204, 217, 370, 373, 374, 379
			T228	MCK1		32, 56, 116, 122, 142, 152, 204, 217, 370, 373, 374, 379
			T232	MCK1		7, 32, 56, 116, 122, 142, 152, 204, 217, 373, 374, 379
SRO9	Cytoplasmic RNA-binding protein; shuttles between nucleus and cytoplasm and is exported from the nucleus in an mRNA export-dependent manner; associates with	S433	S40	CDC28		7, 32, 139, 142, 379

	translating ribosomes; involved in heme regulation of Hap1p as a component of the HMC complex, also involved in the organization of actin filaments; contains a La motif; SRO9 has a paralog, SLF1, that arose from the whole genome duplication					
			T69	PSK2		116, 342, 373
			T71	PSK2		342
GSY2	Glycogen synthase; expression induced by glucose limitation, nitrogen starvation, heat shock, and stationary phase; activity regulated by cAMP-dependent, Snf1p and Pho85p kinases as well as by the Gac1p-Glc7p phosphatase; GSY2 has a paralog, GSY1, that arose from the whole genome duplication; relocalizes from cytoplasm to plasma membrane upon DNA replication stress	S651; S655	S651	MCK1	RIM11	7, 32, 37, 100, 122, 133, 139, 142, 148, 149, 152, 217, 342, 370, 374, 379, 427
			S655	PCL10, PHO85		7, 26, 37, 100, 122, 133, 142, 148, 149, 217, 342, 370, 374, 379, 427
			T668	PCL10, PHO85		26, 133, 148, 149, 427
BMH1	14-3-3 protein, major isoform; controls proteome at post-transcriptional level, binds proteins and DNA, involved in regulation of exocytosis, vesicle transport, Ras/MAPK and rapamycin-sensitive signaling, aggresome formation, spindle position checkpoint; protein increases in abundance and relative distribution to the nucleus increases upon DNA replication stress; antiapoptotic gene similar to human 14-3-3; BMH1 has a paralog, BMH2, that arose from whole genome duplication	T231; T234; S235; S238; S240	S238	HRR25		32, 63, 142, 374, 417

NTH1	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; phosphorylated and activated by Cdc28p at the G1/S phase transition to coordinately regulate carbohydrate metabolism and the cell cycle; inhibited by Dcs1p; NTH1 has a paralog, NTH2, that arose from the whole genome duplication	S83	S20	TPK1	7, 100, 104, 122, 142, 217, 370, 379, 423
			S66	CDC28	7, 32, 56, 100, 104, 142, 152, 370, 374, 379, 423
			S83	TPK1	7, 32, 56, 100, 104, 142, 152, 370, 374, 379, 423
PUP2	Alpha 5 subunit of the 20S proteasome; involved in ubiquitin-dependent catabolism; human homolog is subunit zeta	T55; S56; S251	S56	CDC28	7, 122, 142, 181, 217, 370, 374, 379
NIP1	eIF3c subunit of the eukaryotic translation initiation factor 3 (eIF3); involved in the assembly of preinitiation complex and start codon selection; eIF3 is also involved in programmed stop codon readthrough	S98; S99; S103; S222; T228; T239	S98	TEL1	7, 32, 96, 100, 142, 152, 217, 370, 374, 379
			S99	TEL1	7, 32, 96, 100, 142, 152, 217, 370, 374, 379
			S103	TEL1	7, 32, 96, 100, 142, 152, 217, 370, 374, 379
NUP2	Nucleoporin involved in nucleocytoplasmic transport; binds to either the nucleoplasmic or	T14; S17; S20; S84; S203; S205; S537;	S17	MCK1	7, 32, 56, 100, 116,

	cytoplasmic faces of the nuclear pore complex depending on Ran-GTP levels; also has a role in chromatin organization	S538; S540; T577; S581				142, 152, 217, 369, 373, 374, 379
			S20	MCK1		7, 32, 56, 100, 116, 142, 152, 217, 369, 373, 374, 379
			S68	RAD53		7, 139, 142, 370
			S203	RAD53	PTP1	7, 32, 56, 116, 142, 152, 217, 370, 373, 374
			S205	ALK2	PTP1	7, 32, 56, 116, 142, 152, 217, 370, 373, 374
			S248	RAD53		7, 370
			S284	RAD53		7, 370
			S317	RAD53		7, 370
			S351	RAD53		7, 52, 370
			S368	RAD53		7, 142, 370, 379
			S399	MEC1, TEL1		370, 379
			S512	RAD53		370
			S523	RAD53		370
PAN1	Part of actin cytoskeleton-regulatory complex Pan1p-Sla1p-End3p; associates with actin patches on cell cortex; promotes protein-protein interactions essential for endocytosis; binds to and activates Arp2/3 complex in vitro; phosphorylation of Thr-1225 is regulated by MAPK Hog1p in response to	T570; T993; S1003; S1250; S1253; S1255; T1256	T148	PRK1		147, 395, 453

	osmotic stress; previously thought to be a subunit of poly(A) ribonuclease				
			T170	PRK1	147, 395, 453
			T194	PRK1	147, 395, 453
			T221	PRK1	7, 147, 395, 453
			T241	PRK1	7, 147, 395, 453
			T398	PRK1	147, 395, 453
			T415	PRK1	147, 395, 453
			T428	PRK1	147, 395, 453
			T452	PRK1	147, 395, 453
			T473	PRK1	147, 395, 453
			T504	PRK1	147, 395, 453
			T513	PRK1	147, 395, 453
			T544	PRK1	147, 395, 453
			T551	PRK1	7, 146, 147, 395, 453
			T566	PRK1	7, 32, 142, 146, 147, 152, 395, 453
			T570	PRK1	7, 32, 142, 147, 152, 379, 395, 453
SIP1	Alternate beta-subunit of the Snf1p kinase complex; may confer substrate specificity; vacuolar protein containing KIS (Kinase-	S331	S198	CDC28	7, 142, 217, 379

	Interacting Sequence) and ASC (Association with Snf1 kinase Complex) domains involved in protein interactions					
			S200	CDC28		7, 116, 142, 217, 373, 374, 379
SRP40	Nucleolar serine-rich protein; role in preribosome assembly or transport; may function as a chaperone of small nucleolar ribonucleoprotein particles (snoRNPs); immunologically and structurally to rat Nopp140	S133; T141	S133		SIW14	32, 56, 116, 152, 373
YSC84	Actin-binding protein; involved in bundling of actin filaments and endocytosis of actin cortical patches; activity stimulated by Las17p; contains SH3 domain similar to Rvs167p; YSC84 has a paralog, LSB3, that arose from the whole genome duplication	Y296; S301	S311			7, 32, 142, 217, 374, 379
SPC29	Inner plaque spindle pole body (SPB) component; links the central plaque component Spc42p to the inner plaque component Spc110p; required for SPB duplication	S216	S39			32, 116, 373
			S40			32, 116, 373
			S59			32, 56, 142, 374, 379
			S70			32, 116, 373
			T240			7, 15, 37, 56, 116, 141, 142, 164, 373
MKS1	Pleiotropic negative transcriptional regulator; involved in Ras-CAMP and lysine biosynthetic pathways and nitrogen regulation; involved in retrograde (RTG) mitochondria-to-nucleus signaling	S440; S442	S217	FRK1		7, 32, 139
EDE1	Scaffold protein involved in the formation of early endocytic sites; putative regulator of cytokinesis; homo-oligomerization is required for localization to and organization of	S241; S931; S1006; S1008; S1011; S1012; T1065; S1093; S1095;	S241		PTC4	7, 32, 100, 122, 142, 152, 217,

	endocytic sites; has a network of interactions with other endocytic proteins; binds membranes in a ubiquitin-dependent manner; may also bind ubiquitinated membrane-associated proteins; interacts with Cmk2 and functions upstream of CMK2 in regulating non-apoptotic cell death; homolog of mammalian Eps15	S1096; S1100; S1104; T1160; T1178; S1179; S1181; S1187; T1307; S1309				370, 374, 379
			S244		PTC4	7, 32, 100, 122, 142, 152, 217, 374, 379
			S249		PTC4	7, 32, 142, 152, 217, 374, 379
			S527		PSR2	32, 152, 370
			S1069		CMP2	7, 32, 142, 379
			S1096	FUS3		7, 32, 56, 116, 142, 152, 217, 370, 373, 374, 379
			S1100	PHO85		7, 32, 56, 100, 116, 142, 152, 217, 370, 373, 374, 379
			T238	CDC28		7, 32, 100, 122, 142, 152, 217, 370, 374, 379
			T1072		CMP2	7, 32, 142, 379
PIN4	Protein involved in G2/M phase progression and response to DNA damage; interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ	T512; S538; S541; S545; S653; S655	S466	CDC28		7, 32, 116, 122, 139, 142, 217,

	cluster domains; hyperphosphorylated in response to DNA damage						373, 374, 379
			S541	CDC28			32, 122, 142, 152, 379
			S653			SIT4	7, 32, 37, 116, 122, 142, 370, 373, 374, 379
			S655			SIT4	7, 32, 116, 122, 142, 370, 373, 374, 379
SHP1	UBX domain-containing substrate adaptor for Cdc48p; ubiquitin regulatory X domain-containing protein that acts as a substrate recruiting cofactor for Cdc48p; positively regulates Glc7p PPase activity to promote growth and mitotic progression in complex with Cdc48p; ubiquitinated protein interactor involved in ER-associated degradation (ERAD); regulated by nuclear Ub-dependent degradation (INMAD pathway) independent of the Asi and Doa10 complexes; homolog of human p47 (NSFL1C)	S97; S106; T107; S115; S224; S315; S321; S322; T331	S106	KNS1			7, 32, 100, 116, 152, 373, 379
			S108	PTK1			7, 32, 100, 116, 152, 370, 373, 379
			S315	CDC28	CDC28		7, 32, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S322	CDC28			7, 32, 139, 142, 217, 374, 379

GCS1	ADP-ribosylation factor GTPase activating protein (ARF GAP); involved in ER-Golgi transport; required for prospore membrane formation; regulates phospholipase Spo14p; shares functional similarity with Glo3p; GCS1 has a paralog, SPS18, that arose from the whole genome duplication	S149; T151; S157; T161; S168; T170	S157	CKA1		7, 32, 142, 217, 370, 374, 379
			T151	MCK1		7, 32, 142, 152, 217, 370, 374
			T161	CDC28		7, 32, 139, 142, 217, 370, 374, 379
			T170	CLB2, CDC28		7, 32, 100, 142, 370, 379
DEF1	RNAPII degradation factor; forms a complex with Rad26p in chromatin, enables ubiquitination and proteolysis of RNAPII present in an elongation complex; mutant is deficient in Zip1p loading onto chromosomes during meiosis	T258; S260; S307	S273	RAD53		56, 116, 370
BDF1	Protein involved in transcription initiation; functions at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p; BDF1 has a paralog, BDF2, that arose from the whole genome duplication	S270; S612; S613; S615; T617	S630	MEC1, TEL1		52, 379
EAP1	eIF4E-associated protein, competes with eIF4G for binding to eIF4E; accelerates mRNA degradation by promoting decapping, facilitated by interaction with eIF4E; essential for Puf5p mediated repression; associates with Puf5p and Dhh1p; inhibits cap-dependent translation; functions independently of eIF4E to maintain genetic stability; plays a role in	S389; S390; T391	S363		PSR1	32, 142

	cell growth, implicated in the TOR signaling cascade					
			S387	MCK1		7, 32
ELF1	Transcription elongation factor with a conserved zinc finger domain; implicated in the maintenance of proper chromatin structure in actively transcribed regions; deletion inhibits Brome mosaic virus (BMV) gene expression	S124; S142	S117	PSK2		7, 32, 116, 142, 193, 217, 370, 373, 374, 379
			S124	PSK2		7, 32, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
SPC42	Central plaque component of spindle pole body (SPB); involved in SPB duplication, may facilitate attachment of the SPB to the nuclear membrane	T357; T359	T357	MPS1		37, 142, 379
YRO2	Protein with a putative role in response to acid stress; null mutant is sensitive to acetic acid; transcription is regulated by Haa1p and induced in the presence of acetic acid; protein observed in plasma membrane foci in the presence of acetic acid; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies	T341; S343	S297		SIW14	32, 142
			S299		SIW14	7, 32, 142, 370, 379
HEK2	RNA binding protein involved in asymmetric localization of ASH1 mRNA; represses translation of ASH1 mRNA, an effect reversed by Yck1p-dependent phosphoryation; regulates telomere position effect and length; similarity to hnRNP-K	S252; S358; S360; S362	S252		YVH1	7, 32, 301, 370, 374, 379
			S358	YCK1		7, 56, 142, 217, 301, 370, 374

			S360	YCK1	7, 142, 217, 301, 370, 374
			S362	YCK1	7, 142, 301, 370, 379
			S381	YCK1	7, 32, 139, 142, 301, 374
			T352	YCK1	301
			T355	YCK1	56, 142, 301, 374
IST2	Cortical ER protein involved in ER-plasma membrane tethering; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to the plasma membrane (PM) and regulate PM phosphatidylinositol-4-phosphate (PI4P) levels by controlling access of Sac1p phosphatase to its substrate PI4P in the PM; localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process	T701; S704; T712; S714; T726; S729; Y730; T736; S757; S763; S764; S767; S768; S844; S847; T850; T853	S764	CTK1	32, 374
			S767	YPK1	7, 32, 374, 379
TPS3	Regulatory subunit of trehalose-6-phosphate synthase/phosphatase; involved in synthesis of storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway; TPS3 has a paralog, TSL1, that arose from the whole genome duplication	S51; S52; T55; S56; S58; S59; Y61; S148; S150; S154; S181; S195	S148	CDC28	7, 32, 122, 142, 152, 217, 374, 379
TSL1	Large subunit of trehalose 6-phosphate synthase/phosphatase complex; Tps1p-Tps2p complex converts uridine-5'-diphosphoglucose and glucose 6-phosphate to trehalose; contributes to survival to acute lethal heat stress; mutant has aneuploidy tolerance; protein abundance increases in response to DNA replication stress; TSL1 has a paralog,	S49; S53; S56; S71; S73; S77; S79; S85; S86; T87; T88; T115; S118; S135; S137; S138; S147; S155; S157; S161; S186; T191; S192; T194; S195; T205;	S49	CKA1	7, 32, 122, 142, 379

	TPS3, that arose from the whole genome duplication	T215; S216; T219; S220					
			S77	CDC28	CDC28		7, 32, 100, 122, 139, 142, 370, 374, 379
			S79	MCK1			7, 32, 142, 370
			S135	CDC28	CDC28		7, 32, 139, 142, 370, 374
			S147	CDC28	CDC28		7, 32, 139, 142, 370, 374, 379
			S155	MCK1			32, 142
			S157	MCK1			7, 32, 122, 139, 142, 374
			S161	CDC28	CDC28		7, 32, 122, 139, 142, 374, 379
LEO1	Component of the Paf1 complex; which associates with RNA polymerase II and is involved in histone methylation; plays a role in regulating Ty1 transposition; involved in transcription elongation as demonstrated by the G-less-based run-on (GLRO) assay	S132; S358; S372; T374	S34	MEC1, TEL1			7, 142, 217, 370
			S132			CMP2	7, 32, 116, 142, 217, 373, 379
			S339	MEC1, TEL1			7, 32, 52, 139, 142, 217, 370, 374, 379
SIC1	Cyclin-dependent kinase inhibitor (CKI); inhibitor of Cdc28-Clb kinase complexes that controls G1/S phase transition, preventing premature S phase and ensuring genomic integrity; phosphorylated by Clb5/6-Cdk1 and Cln1/2-Cdk1 kinase which regulate timing of	S191	S69				33, 188, 262, 283, 287, 295, 414

Sic1p degradation; phosphorylation targets Sic1p for SCF(CDC4)-dependent turnover; functional homolog of mammalian Kip1			
	S76		33, 188, 261, 262, 283, 287, 295, 414, 441
	S80		37, 188, 262, 283, 414
	S145		37, 97, 122, 283, 295, 354, 414
	S191		7, 32, 37, 116, 122, 139, 142, 152, 272, 283, 373, 374, 414
	S201		7, 23, 37, 61, 64, 65, 116, 139, 142, 217, 374, 379
	T2	CDC28	33, 139, 283, 287, 295, 414
	T5		7, 139, 283, 287, 414
	T33		37, 97, 262, 283, 287, 354, 413, 414
	T45		37, 97, 262, 354, 379
	T48		33, 261, 262, 283, 295, 354, 414

			T173			7, 32, 90, 97, 116, 122, 152, 217, 272, 273, 283, 295, 373, 414, 461
YHR097C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus; YHR097C has a paralog, PAL1, that arose from the whole genome duplication	S221; S222; T223; T224; T225; S233	S222		YVH1	7, 32, 100, 116, 217, 370, 373, 379
			S315	PTK1		7, 32, 56, 116, 142, 152, 373, 379
			T313		PPQ1	7, 32, 56, 116, 142, 152, 373, 379
BZZ1	SH3 domain protein implicated in regulating actin polymerization; able to recruit actin polymerization machinery through its SH3 domains; colocalizes with cortical actin patches and Las17p; interacts with type I myosins	S472	S472	SNF1		7, 32, 142, 374, 379
UME6	Rpd3L histone deacetylase complex subunit; key transcriptional regulator of early meiotic genes; involved in chromatin remodeling and transcriptional repression via DNA looping; binds URS1 upstream regulatory sequence, represses transcription by recruiting conserved histone deacetylase Rpd3p (through co-repressor Sin3p) and chromatin-remodeling factor Isw2p; couples metabolic responses to nutritional cues with initiation and progression of meiosis, forms compl	S316; S318; S321; T403	S107	MCK1, MRK1, RIM11		32, 142, 379, 436
			S316	FRK1		7, 32, 142, 152, 217, 379

			T99	MCK1, MRK1, RIM11			32, 142, 244, 379, 436
			T103	MCK1, MRK1, RIM11			32, 379, 436
ZRG8	Protein of unknown function; authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; GFP-fusion protein is localized to the cytoplasm; transcription induced under conditions of zinc deficiency	S676	S365				32, 56
			S914				142, 379
YER079W	Putative protein of unknown function	T31; S39; S41; Y186; S189; S192; S194; S197; T201	S39		RIM11	SIT4	7, 32, 139, 142, 374
			S41	CDC28		SIT4	7, 32, 142, 374, 379
			S189	TPK3			7, 32, 142, 370, 379
			S192	TPK3			7, 32, 142, 370, 379
			S194	CKA1			7, 32, 142, 379
			T53			SIT4	7, 32, 142, 217, 374
VHS2	Regulator of septin dynamics; involved in the regulation of septin dynamics at bud neck after mitotic entry, likely by stabilizing septin structure; regulated at post-translational level by cell cycle dependent phosphorylation; likely phosphorylated by Cdc28p and dephosphorylated by Cdc14p before cytokinesis; high-copy suppressor of synthetic lethality of sis2 sit4 double mutant; VHS2 has a paralog, MLF3, that arose from the whole genome duplication		S202			SIT4	32, 142
			S301	CDC28	CDC28		7, 139, 142, 152, 217, 374, 379

			S325			PTP1	32, 142, 152, 217
			S330			PTP1	32, 142, 152
YRB2	Protein of unknown function; involved in nuclear processes of the Ran-GTPase cycle; involved in nuclear protein export; contains Ran Binding Domain and FxFG repeats; interacts with Srm1p, GTP-Gsp1p, Rna1p and Crm1p; relocalizes to the cytosol in response to hypoxia; not essential for viability	T117; T123; T124; S125; T126; S128	S14				7, 116, 142, 370, 373
			T31				7, 32, 139, 142, 370, 374, 379
AIM21	Protein of unknown function; involved in mitochondrial migration along actin filament; may interact with ribosomes; GFP-fusion protein colocalizes with Sac1p to the actin cytoskeleton	S36; T40; T84; S119; T121; T180; S183; S185; S281; T282; S476; S477; T480; T552	S183	PSK2			7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			T180	PSK2			7, 32, 142, 152, 217, 370, 374, 379
GLC8	Regulatory subunit of protein phosphatase 1 (Glc7p); involved in glycogen metabolism and chromosome segregation; proposed to regulate Glc7p activity via conformational alteration; ortholog of the mammalian protein phosphatase inhibitor 2; protein abundance increases in response to DNA replication stress	S184	S158	FRK1			7, 32, 116, 139, 142, 217, 373
YPI1	Regulatory subunit of the type I protein phosphatase (PP1) Glc7p; Glc7p participates in the regulation of a variety of metabolic processes including mitosis and glycogen metabolism; in vitro evidence suggests Ypi1p is an inhibitor of Glc7p while in vivo evidence suggests it is an activator; overproduction causes decreased cellular content of glycogen; partial depletion causes lithium sensitivity,	S133	S131	PSK1	CLA4		7, 32, 37, 56, 116, 139, 142, 217, 370, 373, 374

	while overproduction confers lithium-tolerance				
			S133	PSK1	7, 32, 37, 56, 116, 122, 142, 217, 370, 373, 374, 379
IGD1	Cytoplasmic protein that inhibits Gdb1p glycogen debranching activity; required for normal intracellular accumulation of glycogen; phosphorylated in vivo; expression increases during wine fermentation; protein abundance increases in response to DNA replication stress; IGD1 has a paralog, YOL024W, that arose from the whole genome duplication	S14	S95	TPK3	7, 32, 100, 142, 370
CKB1	Beta regulatory subunit of casein kinase 2 (CK2); a Ser/Thr protein kinase with roles in cell growth and proliferation; CK2, comprised of CKA1, CKA2, CKB1 and CKB2, has many substrates including transcription factors and all RNA polymerases	S111	S111	RIO1	7, 32, 152, 370
FYV8	Protein of unknown function; required for survival upon exposure to K1 killer toxin	S666	S92		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			S100		7, 32, 116, 122, 142, 152, 217, 370, 373, 374, 379
NET1	Core subunit of the RENT complex; involved in nucleolar silencing and telophase exit; stimulates transcription by RNA polymerase I and regulates nucleolar structure; NET1 has a paralog, TOF2, that arose from the whole genome duplication	S231	S30	CDC5	363
			S31	CDC5	363

	S48	CDC5		236, 363, 379
	S56	CDC5		37, 152, 236, 363
	S60	CDC5		37, 142, 152, 236, 363, 379
	S64	CDC5		152, 236, 363, 379
	S166	CDC28		20, 32, 116, 142, 152, 373, 379
	S169	CDC28		32, 152
	S223	CDC5		363
	S224	CDC5		7, 139, 152, 363, 374
	S228	CDC5	CKA2	7, 37, 139, 142, 152, 236, 363, 374, 379
	S231	CDC5		7, 20, 37, 142, 152, 217, 236, 363, 374, 379
	S242	CDC5		32, 152, 236, 363, 379
	S252	CDC28		7, 20, 32, 37, 122, 142, 152, 236, 379
	S259	CDC5		20, 32, 152, 236, 379
	S269	CDC5		152, 236, 379
	S280	CDC5		236

	S295	CDC5	SNF1	139, 142, 152, 363, 379
	S301	CDC5		363
	S335	CDC5		363
	S447	CLB2, CDC28		32, 37, 142, 379
	S452	CLB2, CDC28		7, 32, 37, 56, 122, 142, 152, 217, 370, 374
	S830	CDC28		7, 32, 37, 142
	S840	RAD53		7, 37, 56, 370, 379
	S1032	CLB2, CDC28	CDC28	7, 20, 32, 116, 139, 142, 217, 373, 374, 379
	S1056	CLB2, CDC28		7, 32, 37, 142, 152, 379
	T16	CDC5		363
	T192	CDC5		236, 363
	T194	CDC5		363
	T195	CDC5		363
	T196	CDC5		363
	T197	CDC5		363
	T288	CDC5		139, 142, 152, 236, 363
	T297	CDC28		142, 152, 363, 379
	T302	CDC5		152, 363
	T676	CLB2, CDC28		20, 32, 56, 142, 152,

						217, 374, 379
			T1042	CLB2, CDC28		7, 32, 37, 142, 152, 370, 379
BBC1	Protein possibly involved in assembly of actin patches; interacts with an actin assembly factor Las17p and with the SH3 domains of Type I myosins Myo3p and Myo5p; localized predominantly to cortical actin patches	S77; S78; T81; S83; S103; S158; S620; S621; T624; T810; S815; T818; T820; S822; T824; T835; T894; T895; S902	S103	CDC28	PHO85	7, 32, 56, 116, 139, 142, 217, 370, 373, 374, 379
			S631	MKK1		7, 32, 122, 142, 152, 217, 379
			S634	MKK1		7, 32, 142, 152, 217, 379
			S638	MKK1		32, 116, 122, 142, 152, 217, 373, 379
			T636	MKK1		32, 116, 122, 142, 152, 373, 379
PTK2	Serine/threonine protein kinase; involved in regulation of ion transport across plasma membrane; carboxyl terminus is essential for glucose-dependent Pma1p activation via phosphorylation of Pma1p-Ser899; enhances spermine uptake; PTK2 has a paralog, PTK1, that arose from the whole genome duplication	T56; S57; S59; S61; S63; S65; S69; S73; S585; T586; S587; T588; S592; S595; S711; S726; T727; T729; T730; T732; S773; S775; S776	S69	CLB2, CDC28		37, 56, 142, 152, 379
			S711	PTK2	CKA2	7, 32, 37, 139, 142, 217, 374, 379
			S752	PTK2		7, 32, 116, 142, 217, 373, 374, 379

			S755	PTK2		32, 142, 217, 379
			S784	CLB2, CDC28		7, 32, 37, 142, 379
			T727	CDC28		7, 37, 116, 142, 217, 373
			T730	CDC28		7, 37, 116, 142, 217, 373, 379
			T737	CDC28		7, 32, 116, 142, 217, 373, 374, 379
ASK10	Regulator of the Fps1p glycerol channel; under nonstress conditions, binds to Fps1p to positively regulate glycerol transport; under osmotic stress, multiple phosphorylation by Hog1p causes Ask10p to dissociate from Fps1p; forms homodimers and heterodimerizes with paralog Rgc1p; phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p; associates with RNA polymerase II holoenzyme	S1070	T808	CDC28		7, 32, 37, 142, 152, 379
SKP1	Evolutionarily conserved kinetochore protein; part of multiple protein complexes, including the SCF ubiquitin ligase complex, the CBF3 complex that binds centromeric DNA, and the RAVE complex that regulates assembly of the V-ATPase; protein abundance increases in response to DNA replication stress	S45; S49	S45	PHO85		32, 142, 152, 379
			S47	PHO85		32, 142, 152, 379
			S49	PTK1		32, 142, 152, 379
			T3	MPS1		37
EDC1	RNA-binding protein that activates mRNA decapping directly; binds to mRNA substrate and enhances activity of decapping proteins Dcp1p and Dcp2p; has a role in translation	S82	S82		PTP1	7, 32, 56, 116, 142, 370, 373, 374, 379

	during heat stress; protein becomes more abundant and forms cytoplasmic foci in response to DNA replication stress; EDC1 has a paralog, EDC2, that arose from the whole genome duplication						
			S85			PTP1	32, 56, 116, 142, 370, 373, 374, 379
SDS23	Protein involved in cell separation during budding; one of two S. cerevisiae homologs (Sds23p and Sds24p) of the S. pombe Sds23 protein, which is implicated in APC/cyclosome regulation; SDS23 has a paralog, SDS24, that arose from the whole genome duplication	S61; T66; S398; S399; S400; S402; S404; T405; T409; T410; S430	T405	CDC28			142, 217, 379
YGR054W	Eukaryotic initiation factor eIF2A; associates specifically with both 40S subunits and 80 S ribosomes, and interacts genetically with both eIF5b and eIF4E; homologous to mammalian eIF2A	S473; S560; S561; T563; S564; S567; T568; S572; T581; T586; S587	S560	MCK1	TPK1		7, 32, 139, 142, 370, 374
			S561	MCK1			7, 32, 142, 370, 374
			S564	MCK1			7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			T563	MCK1			7, 32, 116, 142, 152, 217, 370, 373, 374
			T568	MCK1			7, 32, 142, 379
YGR130C	Component of the eisosome with unknown function; GFP-fusion protein localizes to the cytoplasm; specifically phosphorylated in vitro by mammalian diphosphoinositol pentakisphosphate (IP7)	S44; S249; T254; S257; T277; T278; S281; S284; S286; T337; S338; T339; T342	S343	TPK3			32, 217, 370, 379

			S347	YPK1		32, 217, 370, 379
MDG1	Plasma membrane protein; involved in G-protein mediated pheromone signaling pathway; overproduction suppresses bem1 mutations; MDG1 has a paralog, CRP1, that arose from the whole genome duplication	S160; T164; S178; T180; T181; T182; S227; T256; S257; S263; S272	S288	CKA1		7, 32, 116, 122, 142, 152, 373, 374, 379
			S291	PSK2		7, 32, 116, 122, 142, 373, 374, 379
			T290	PSK2		7, 32, 116, 122, 142, 152, 373, 374
BNI5	Linker protein responsible for recruitment of myosin to the bud neck; interacts with the C-terminal extensions of septins Cdc11p and Shs1p and binds Myo1p to promote cytokinesis	S263; S270; S273; T274; T280	S270		SNF1	7, 32, 100, 139, 142, 217, 280, 370, 374, 379
			S273			7, 32, 100, 142, 217, 280, 281, 370, 379
			T274			7, 32, 100, 142, 280, 370, 379
NSG2	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; NSG2 has a paralog, NSG1, that arose from the whole genome duplication	S49; S81; S82	S90	YPK1		7, 32, 100, 142, 152, 217, 370, 374, 379
			S92	YPK1		7, 32, 100, 142, 152, 217, 370, 374, 379
			S93	YPK1		7, 32, 100, 142, 152,

					217, 370, 374, 379
CRZ1	Transcription factor, activates transcription of stress response genes; nuclear localization is positively regulated by calcineurin-mediated dephosphorylation; rapidly localizes to the nucleus under blue light stress; can be activated in stochastic pulses of nuclear localization in response to calcium		S409	TPK1	142, 170, 370
			S410	TPK1	142, 170, 370, 379
			S423	TPK1	32, 56, 170
			S427	TPK1	7, 32, 56, 170, 379
			S429	TPK1	7, 32, 170, 379
GPD1	NAD-dependent glycerol-3-phosphate dehydrogenase; key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high-osmolarity glycerol response pathway; protein abundance increases in response to DNA replication stress; constitutively inactivated via phosphorylation by the protein kinases Ypk1p and Ypk2p, dephosphorylation increases catalytic activity; forms a heterodimer with Pnc1p to facilitate its peroxisomal import	S23; S24; S25; S27	S24	CTK1	7, 32, 100, 116, 122, 142, 152, 168, 217, 294, 370, 373, 379
			S27	CTK1	7, 32, 100, 116, 122, 142, 152, 168, 217, 294, 370, 373, 374, 379
REG1	Regulatory subunit of type 1 protein phosphatase Glc7p; involved in negative regulation of glucose-repressible genes; involved in regulation of the nucleocytoplasmic shuttling of Hxk2p; REG1	S254; Y497; S570; S572; S576; T579; S582; S775; T776; S778; Y780; S976; S977; S1013; S1014	S421	CDC28	7, 32, 37, 56, 142, 217, 370, 379

	has a paralog, REG2, that arose from the whole genome duplication						
			S898	CDC28			7, 142, 379
			T896	CDC28			142, 379
CUE4	Protein of unknown function; has a CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; CUE4 has a paralog, CUE1, that arose from the whole genome duplication	T32; S41; S48; S54	S48	KNS1			7, 32, 142, 370, 379
SEG1	Component of eisosome required for proper eisosome assembly; precedes Pil1p/Lsp1p during eisosome formation, controls eisosome length and shape; diffusely distributed, forms heterogeneous patches at plasma membrane in small buds, also found in medium and large buds; expression repressed by cAMP; similar to A. gossypii SEG gene and to S. pombe Sle1p, important for generating eisosomes; SEG1 has a paralog, SEG2, that arose from the whole genome duplication	S302; S318; S450; T452	S658	CLB2, CDC28			7, 142, 379
			S870	CDC28			32, 142
			T675	CLB2, CDC28			7, 32, 56, 142, 370, 374, 379
TRI1	Non-essential sumoylated protein of unknown function; similar to components of human SWI/SNF complex including SMRD3; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, nucleus and nucleolus; TRI1 has a paralog, UAF30, that arose from the whole genome duplication	S113	S113	CDC28	CDC28		7, 139, 142, 379
EIS1	Component of the eisosome required for proper eisosome assembly; similar to Uso1p; authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies; protein increases in abundance and relocalizes from plasma membrane to cytoplasm upon DNA replication stress; EIS1 has a paralog,	T18; S19; S23; S26; S130; S133; S151; S179; S584; S701; Y704; T706; S710; T759; T761; S762; S763; T767; S775; S780; S781; S791; S795; S825; S828; S829; S838	S23			SIW14	32, 56, 116, 142, 370, 373, 379

	YKL050C, that arose from the whole genome duplication					
			S30		SIW14	32
			S130	MCK1 SCH9		7, 32, 56, 116, 139, 142, 152, 331, 373, 374, 379
			S133	MCK1		7, 32, 56, 116, 152, 373, 379
			S136	SNF1		32, 116, 152, 373, 379
			S139	SNF1		32, 56, 379
			S584	YPK1 TPK1		7, 32, 56, 116, 122, 139, 142, 217, 370, 373, 374, 379
			S762	PSK2	YVH1	7, 32, 116, 142, 370, 373, 374
			S763	PKP1	YVH1	7, 32, 116, 142, 152, 370, 373, 374, 379
			S775	CKA1 HRR25		7, 32, 116, 139, 142, 152, 370, 373, 379
			S791	FRK1		32, 142
			T767	PSK2		7, 32, 116, 139, 142, 152, 370, 373, 379
MSC3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; msc3 mutants	S80; S82; S83; T144; S151; S155; Y357; S363; T646;	S46	CDC28		142

	are defective in directing meiotic recombination events to homologous chromatids; potential Cdc28p substrate; protein abundance increases in response to DNA replication stress	S648; S658; S659; S660					
FPR4	Peptidyl-prolyl cis-trans isomerase (PPIase); nuclear proline isomerase; affects expression of multiple genes via its role in nucleosome assembly; catalyzes isomerization of proline residues in histones H3 and H4, which affects lysine methylation of those histones; PPIase domain acts as a transcriptional repressor when tethered to DNA by lexA, and repressor activity is dependent on PPIase activity; contains a nucleoplasmin-like fold and can form pentamers	S80; S82	S80	KIN28	CKA2		7, 32, 37, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
			S82	KIN28	CKA2		7, 32, 37, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
BCP1	Essential protein involved in nuclear export of Mss4p; Mss4p is a lipid kinase that generates phosphatidylinositol 4,5-biphosphate and plays a role in actin cytoskeleton organization and vesicular transport	T205	T205		CKA2	SIT4	7, 32, 116, 139, 142, 152, 217, 370, 373, 374
CRN1	Coronin; cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; plays a role in regulation of actin patch assembly	S456; S460; S462; S463; S465; S484; S485; T520; T565; S567; S573; T575; S578; S579; T600; S601	S463			PPH21	7, 32, 56, 116, 142, 217, 370, 373, 374, 379
SPN1	Protein involved in RNA polymerase II transcription; is constitutively recruited to the CYC1 promoter and is required for recruitment of chromatin remodeling factors for the expression of CYC1 gene; interacts genetically or physically with RNAP II, TBP, TFIIS, and chromatin remodelling factors;	T15; S85; T86; S89; T120	S23	MEC1, TEL1			7, 32, 52, 116, 142, 152, 217, 370, 373, 374, 379

	central domain highly conserved throughout eukaryotes; mutations confer an Spt- phenotype					
			S89	SSK2		7, 32, 56, 116, 142, 192, 217, 370, 373, 374, 379
			S118	KNS1		32, 370, 379
HBT1	Shmoo tip protein, substrate of Hub1p ubiquitin-like protein; mutants are defective for mating projection formation, thereby implicating Hbt1p in polarized cell morphogenesis; HBT1 has a paralog, YNL195C, that arose from the whole genome duplication	Y29; S41; S43; T45; S251; T259; S301; S303; Y362; S363; S427; Y428; S431; S795; S843; S850; Y855; S856; S857; S932; T939; T940; S941; Y942; S943; T948; T949; S950; S956; S959; S962; S983; S990; T991; S993; Y1003; S1005; S1036	S41	SAT4		7, 32, 116, 142, 373
			S43	PBS2		32, 116, 142, 373
			S251		SIW14	32
			S257		SIW14	32
			S301	PSK2		32, 142, 370, 374
			S303	MCK1		32, 142, 370, 374
			S363	PKP1	PPH22	7, 32, 56, 116, 142, 370, 373
			S561		PPH22	32, 142
			S671	CDC28	PPS1	32, 142
			S856	PKP1		32, 142, 374
			S857	MCK1	PPH22	32, 142, 374
			S956	MCK1		7, 32, 100, 116, 142,

						370, 373, 374
			S959	MCK1	PPH22	32, 100, 116, 142, 373, 374
			S962	PKP1	PPH22	32, 100, 116, 142, 373, 374
			S990	CMK1		32
			S1034	PKP1	CLA4	7, 32, 116, 122, 139, 142, 217, 373
			S1036	CLA4	PPH22	7, 32, 116, 122, 142, 373
			T366	PSK2		7, 32, 370
			T368	PKP1		32
			T949	PBS2		32
			T991	PKP1		32, 56, 100, 142
			T997	MCK1		32, 56, 100, 142, 370
			Y362	PBS2		7, 32, 56, 116, 142, 370, 373
			Y987	MCK1		32
CUE5	Ubiquitin-binding protein; functions as ubiquitin-Atg8p adaptor in ubiquitin-dependent autophagy; serves as proteaphagy receptor for inactivated 26S proteasomes; contains CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; CUE5 has a paralog, DON1, that arose from the whole genome duplication; human TOLLIP is a functional CUE-domain homolog, can complement yeast null mutant, rescuing hypersensitivity of cue5 null mutant cells to Htt-96Q	S21; S36; S45; T50; T70; S220; T346; S348; S351; T352	S21	MKK1		7, 32, 116, 142, 217, 370, 373, 379

			S220	KSP1		7, 32, 142, 217, 374, 379
			T364	CLB2, CDC28		7, 32, 100, 116, 142, 152, 217, 370, 373, 379
			T367	CDC28		7, 32, 100, 142, 152, 370, 379
			T369	CDC28		7, 32, 152
RCN2	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; phosphorylated in response to alpha factor; protein abundance increases in response to DNA replication stress	S102; S104; T105; S110; S129; T132; S149; S150; S152; S156; S157; S160; S183; S185; S186; S187; S188; T189; T200; S201; S204; T248; S250; S255; S257; T259	S143	SLT2		32, 139
			S150	SLT2	RIM11	7, 32, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S152	TPK2		7, 32, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S157	TPK2		7, 32, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379

			S160	SLT2			7, 32, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			T132	TPK2			7, 32, 142, 217, 370
CHS5	Component of the exomer complex; the exomer which also contains Csh6p, Bch1p, Bch2p, and Bud7, is involved in the export of select proteins, such as chitin synthase Chs3p, from the Golgi to the plasma membrane; interacts selectively with the activated, GTP-bound form of Arf1p; Chs5p is the only protein with a BRCT domain that is not localized to the nucleus	S312; S318; S321; S338; S347; T348; S365; T373; S384; S399; S400; S579; S590; S600	S347			SIT4	32, 370
			T334			SIT4	7, 32, 142, 370, 379
MRH1	Protein that localizes primarily to the plasma membrane; also found at the nuclear envelope; long-lived protein that is asymmetrically retained in the plasma membrane of mother cells; the authentic, non-tagged protein is detected in mitochondria in a phosphorylated state; null mutation confers sensitivity to acetic acid	S289; T295; S299	S289	YPK1	CDC28	SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
			T295	PSK2	CDC28	SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
DCS2	m(7)GpppX pyrophosphatase regulator; non-essential, stress induced regulatory protein; modulates m7G-oligoribonucleotide metabolism; inhibits Dcs1p; regulated by Msn2p, Msn4p, and the Ras-cAMP-cAPK signaling pathway; mutant has increased	S58; S60; S63; T64; T340; S341	S63	PKH2			7, 32, 142, 370, 374

	aneuploidy tolerance; DCS2 has a paralog, DCS1, that arose from the whole genome duplication						
			T64	MCK1			7, 32, 116, 142, 370, 373, 374
MSL5	Component of commitment complex; which defines first step in splicing pathway; essential protein that interacts with Mud2p and Prp40p, forming a bridge between the intron ends; also involved in nuclear retention of pre-mRNA; relocalizes to the cytosol in response to hypoxia	S93; S95; S376; S378	S376	CDC28			7, 32, 142, 152, 370, 379
			S378	CDC28			7, 32, 142, 152, 370, 379
BUG1	Cis-golgi localized protein involved in ER to Golgi transport; forms a complex with the mammalian GRASP65 homolog, Grh1p; mutants are compromised for the fusion of ER-derived vesicles with Golgi membranes	S2; S87; T275; T277	S87	CKA2			7, 32, 116, 139, 142, 217, 370, 373, 374, 379
			T277	CDC28			142, 379
HSP42	Small heat shock protein (sHSP) with chaperone activity; forms barrel-shaped oligomers that suppress unfolded protein aggregation; involved in cytoskeleton reorganization after heat shock; protein abundance increases and forms cytoplasmic foci in response to DNA replication stress	S182; S213; S214; S215; S223; S232; T236	S213	PBS2	TPK1		7, 32, 139, 142, 152, 217, 370, 379
			S214	PBS2	SNF1	PPH21	7, 32, 116, 122, 139, 142, 152, 217, 370, 373, 379
			S215			PPH21	7, 32, 116, 122, 142, 152, 217, 370, 373, 379

			S223			PPH21	7, 32, 142, 379
WHI5	Repressor of G1 transcription; binds to SCB binding factor (SBF) at SCB target promoters in early G1; dilution of Whi5p concentration during cell growth determines cell size; phosphorylation of Whi5p by the CDK, Cln3p/Cdc28p relieves repression and promoter binding by Whi5, and contributes to both the determination of critical cell size at START and cell fate; periodically expressed in G1	T284; S288	S59				7, 32, 68, 116, 122, 142, 152, 370, 373, 379, 416
			S62				7, 32, 68, 116, 122, 142, 152, 370, 373, 379, 416
			S88				142, 152, 416
			S154				7, 32, 68, 142, 152, 379, 384, 416
			S156				7, 32, 68, 142, 152, 370, 379, 384, 416
			S161				7, 32, 68, 142, 152, 370, 379, 384, 416
			T5				68, 189, 416
			T57		CDC28		32, 68, 139, 142, 152, 370, 379, 416
PAR32	Protein of unknown function; hyperphosphorylated upon rapamycin treatment in a Tap42p-dependent manner; green fluorescent protein (GFP)-fusion protein		S36	PHO85	SNF1		7, 32, 37, 116, 122, 139, 142, 152, 217,

	localizes to the cytoplasm; PAR32 is not an essential gene						370, 373, 374, 379
			S39	PHO85			7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S49	PHO85			32, 152
			S131	VPS15			32, 142, 152, 217
			S138			YCH1	32, 37, 142, 152, 217, 370, 374, 379
			S141			YCH1	32, 37, 142, 152, 217, 370, 379
			S148	CLB2, CDC28			7, 32, 142, 152
			S246	CLB2, CDC28	CDC28		7, 32, 116, 122, 139, 142, 152, 217, 373, 374, 379
ENT1	Epsin-like protein involved in endocytosis and actin patch assembly; functionally redundant with Ent2p; binds clathrin via a clathrin-binding domain motif at C-terminus; relocalizes from bud neck to cytoplasm upon DNA replication stress; ENT1 has a paralog, ENT2, that arose from the whole genome duplication	T160; S163	T346	PRK1			7, 56, 116, 146, 370, 373, 374, 379
			T366	PRK1			7, 32, 142, 146, 152, 217, 370, 379
			T395	PRK1			7, 32, 122, 142, 146, 152, 217,

							370, 379, 421
			T415	PRK1			146, 421
			T427	PRK1			142, 146
NCB2	Subunit of a heterodimeric NC2 transcription regulator complex; complex binds to TBP and can repress transcription by preventing preinitiation complex assembly or stimulate activated transcription; homologous to human NC2beta; complex also includes Bur6p	S142; S145; S146	S112				7, 66, 100, 142, 217, 379
IGO2	Protein required for initiation of G0 program; prevents degradation of nutrient-regulated mRNAs via the 5'-3' mRNA decay pathway; phosphorylated by Rim15p; GFP protein localizes to the cytoplasm and nucleus; IGO2 has a paralog, IGO1, that arose from the whole genome duplication		S119		CLA4	PPH22	32, 139, 142, 379
			S122			PPH22	32, 142, 152, 370, 379
			S128	CLB2, CDC28			32, 142, 152, 370, 379

Table 3.6 Phosphorylated proteins and their kinases and phosphatases in high density and low density yeast cells treated with LCA at day 5.

Gene Symbol	Description	PhosphoSite in Sample	PhosphoSite in Literature	Known Kinase	Predicted Kinase	Known Phosphatases	References
CDC19	Pyruvate kinase; functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; regulated via allosteric activation by fructose bisphosphate; CDC19 has a paralog, PYK2, that arose from the whole genome duplication	T372; T376; S377; T378	S22	TPK1			7, 104, 122, 142, 217, 317, 370, 374, 379
			T407	CDC28			7, 142, 379
GPM1	Tetrameric phosphoglycerate mutase; mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis	S116	S116	CTK1			7, 32, 56, 122, 139, 142, 217, 370, 374, 379
RAS2	GTP-binding protein; regulates nitrogen starvation response, sporulation, and filamentous growth; farnesylation and palmitoylation required for activity and localization to plasma membrane; homolog of mammalian Ras proto-oncogenes; RAS2 has a paralog, RAS1, that arose from the whole genome duplication	S225; T226; T227	T240	SNF1			7, 32, 217, 379
HTB1	Histone H2B; core histone protein required for chromatin assembly and chromosome function; nearly identical to HTB2; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates reassembly after DNA replication, transcriptional activation, meiotic DSB formation and H3 methylation		S11	STE20			4, 2005
HHF2	Histone H4; core histone protein required for chromatin assembly and chromosome function; one of two identical histone proteins (see also HHF2); contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity		S2	CKA1, CKA2, CKB1, CKB2			55, 191, 407
			S61	RAD53			7, 52, 142

			S65	RAD53			52, 56, 142
DPS1	Aspartyl-tRNA synthetase, primarily cytoplasmic; homodimeric enzyme that catalyzes the specific aspartylation of tRNA(Asp); class II aminoacyl tRNA synthetase; binding to its own mRNA may confer autoregulation; shares five highly conserved amino acids with human that when mutated cause leukoencephalopathy characterized by hypomyelination with brain stem and spinal cord involvement and leg spasticity (HBSL)	S2; S14; S301	S14			SIT4	7, 32, 370, 379
HXK2	Hexokinase isoenzyme 2; phosphorylates glucose in cytosol; predominant hexokinase during growth on glucose; represses expression of HXK1, GLK1, induces expression of its own gene; antiapoptotic; phosphorylation/dephosphorylation at Ser14 by kinase Snf1p, phosphatase Glc7p-Reg1p regulates nucleocytoplasmic shuttling of Hxk2p; functions downstream of Sit4p in control of cell cycle, mitochondrial function, oxidative stress resistance, chronological lifespan; has paralog HXK1	S15; S158	S15	TPK1	TPK1	GLC7, REG1	7, 10, 11, 29, 32, 100, 122, 138, 139, 142, 152, 179, 190, 324, 374
HTA1	Histone H2A; core histone protein required for chromatin assembly and chromosome function; one of two nearly identical subtypes (see also HTA2); DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p; N-terminally propionylated in vivo	S129	S129	MEC1			52, 85, 100, 116, 134, 183, 379, 404, 409, 435
PMA1	Plasma membrane P2-type H+-ATPase; pumps protons out of cell; major regulator of cytoplasmic pH and plasma membrane potential; long-lived protein asymmetrically distributed at plasma membrane between mother cells and buds; accumulates at high levels in mother cells during aging, buds emerge with very low levels of Pma1p, newborn cells have low levels of Pma1p;		S507	YCK1, YCK2			91

	Hsp30p plays a role in Pma1p regulation; interactions with Std1p appear to propagate [GAR+]						
			S899	PTK2			7, 56, 89, 139, 142, 217, 374, 379
NOT3	Component of the CCR4-NOT core complex, involved in mRNA decapping; involved in transcription initiation and elongation and in mRNA degradation; conserved lysine in human homolog of Not3p and Not5p is mutated in cancers	S304; S316; T319; S324; S325; S326; S344; S347; S348; S441; S442; S446; S450; T454; S798	S450	PHO85	RIM11		7, 32, 100, 116, 139, 142, 152, 217, 373, 374, 379
			T454	PHO85			7, 32, 100, 116, 142, 152, 217, 373, 374, 379
DED1	ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase; required for translation initiation of all yeast mRNAs; binds to mRNA cap-associated factors, and binding stimulates Ded1p RNA-dependent ATPase activity; mutation in human homolog DBY is associated with male infertility; human homolog DDX3X complements ded1 null mutation; DED1 has a paralog, DBP1, that arose from the whole genome duplication		S535	MCK1	RIM11	SIT4	7, 32, 56, 139, 142, 152, 217, 374, 379
			S539	MCK1		SIT4	7, 32, 56, 142, 152, 217, 370, 374, 379
			S541	MCK1			7, 32, 142, 152, 370, 379
			S543	MCK1			7, 32, 56, 139, 142, 152, 379

			S576	MCK1			32, 56, 142, 152, 217, 379
GPH1	Glycogen phosphorylase required for the mobilization of glycogen; non-essential; regulated by cyclic AMP-mediated phosphorylation; phosphorylation by Cdc28p may coordinately regulate carbohydrate metabolism and the cell cycle; expression is regulated by stress-response elements and by the HOG MAP kinase pathway	T31	T9	TPK1			222
			T27	TPK1			222, 223
			T31	TPK1	CLA4		7, 32, 122, 139, 142, 154, 213, 217, 325, 326, 370, 374, 379
SNF1	AMP-activated S/T protein kinase; forms a complex with Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis; regulates nucleocytoplasmic shuttling of Hxk2p; regulates filamentous growth and acts as a non-canonical GEF, activating Arf3p during invasive growth; SUMOylation by Mms21p inhibits its function and targets Snf1p for destruction via the Slx5-Slx8 Ub ligase	T210; T408; S413	T210	ELM1		GLC7, REG1	7, 37, 92, 142, 143, 237, 250, 251, 260, 264, 284, 379, 383
TOP2	Topoisomerase II; relieves torsional strain in DNA by cleaving and re-sealing phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis; required for replication slow zone (RSZ) breakage following Mec1p inactivation; human homolog TOP2A	S2; T3; T1306; T1309; T1314	S1310	KNS1			32, 116, 139, 142, 152, 217, 370, 373, 374, 379

	implicated in cancers, and can complement yeast null mutant						
			S1356	CKA1, CKA2			44, 108, 142, 214
			S1363	CKA1, CKA2			214
			T1250	CDC28			142, 370, 379
			T1314	KNS1	CDC28		32, 116, 139, 142, 152, 217, 370, 373, 374, 379
			T1365	CKA1, CKA2			142, 214
BCY1	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA); PKA is a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation	S68; S70; S74; S77; S79; T129; S130; T131; T144; S145; S147; T150	S70	MCK1			7, 32, 142, 374, 379
			S89	CDC28			142
			S130	KNS1			7, 32, 142, 217, 370, 374
			S147	KIN4			32, 142, 374
			T129	KNS1			7, 32, 142, 217, 370, 374, 379
			T131	KNS1			7, 32, 142, 217, 370, 374, 379
			T144			CNA1	7, 32, 37, 40, 56, 142, 217, 374
CHO1	Phosphatidylserine synthase; functions in phospholipid biosynthesis; catalyzes the reaction CDP-diaclyglycerol + L-serine = CMP + L-1-phosphatidylserine,	S34; T40; S46; S47; S50; T53; T54	S46	TPK1	TPK1		7, 32, 59, 122, 139, 142, 152, 217, 370, 374, 379

	transcriptionally repressed by myo-inositol and choline					
			S47	TPK1		7, 32, 59, 122, 142, 152, 217, 370, 374, 379
FBP1	Fructose-1,6-bisphosphatase; key regulatory enzyme in the gluconeogenesis pathway, required for glucose metabolism; undergoes either proteasome-mediated or autophagy-mediated degradation depending on growth conditions; glucose starvation results in redistribution to the periplasm; interacts with Vid30p	S12; T13; T18	S12	TPK1		126, 142, 247, 332, 333
RPS6A; RPS6B	Protein component of the small (40S) ribosomal subunit; homologous to mammalian ribosomal protein S6, no bacterial homolog; phosphorylated on S233 by Ypk3p in a TORC1-dependent manner, and on S232 in a TORC1/2-dependent manner by Ypk1/2/3p; RPS6B has a paralog, RPS6A, that arose from the whole genome duplication		S232	YPK3		7, 32, 100, 116, 122, 142, 152, 162, 373, 379
SEC7	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors; involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles	S2; T334; S434; S437; S439; S809; T1722; S1723; S1726; S1804	S780	VPS34		7, 32, 142, 217, 374, 379
			S782	VPS34		7, 32, 142, 379
			T1240	CDC28	CDC28	139, 142, 217, 374, 379
SCH9	AGC family protein kinase; functional ortholog of mammalian S6 kinase; phosphorylated by Tor1p and required for TORC1-mediated regulation of ribosome biogenesis, translation initiation, and entry	S288; S289; S290	S711	TOR1		335, 379, 406

	into G0 phase; involved in transactivation of osmostress-responsive genes; regulates G1 progression, cAPK activity and nitrogen activation of the FGM pathway; integrates nutrient signals and stress signals from sphingolipids to regulate lifespan					
			S726	TOR1		7, 32, 37, 116, 142, 152, 217, 335, 373, 374, 379, 406
			S758	TOR1		176, 335, 406
			S765	TOR1		176, 335, 406
			T570	PKH1		7, 37, 46, 150, 176, 275, 315, 335, 370, 379, 406, 415
			T723	TOR1		32, 142, 152, 176, 217, 335, 379, 406
			T737	TOR1		46, 176, 275, 335, 379, 406
CAF20	Phosphoprotein of the mRNA cap-binding complex; involved in translational control; repressor of cap-dependent translation initiation; competes with eIF4G for binding to eIF4E	S91; T99; T101; T102; T104; S105; T106; T111	S58	PSK2		342
			S59	PSK2		342
			S78	FRK1		32, 116, 142, 152, 373, 379
			S91	SLT2	CKA2	7, 32, 116, 139, 142,

						217, 370, 373, 374, 379, 452
			T102	SLT2		7, 32, 116, 122, 142, 217, 370, 373, 374, 379
KIN1	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; KIN1 has a paralog, KIN2, that arose from the whole genome duplication	S660; S663; S764; S937; S938	S660	SNF1		7, 32, 142, 379
			S663	SNF1		7, 32, 142, 370, 379
KIN2	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; KIN2 has a paralog, KIN1, that arose from the whole genome duplication		S24	CDC28, CLB2		7, 37, 142, 379
			S609	CDC28		7, 37, 142, 217, 379
			S643	CDC28		7, 32, 37, 116, 142, 370, 373, 374, 379
ABF1	DNA binding protein with possible chromatin-reorganizing activity; involved in transcriptional activation, gene silencing, and DNA replication and repair	S467; S720	S193	MEC1, TEL1		7, 32, 142, 370, 379
			S720	CKA1, CKA2, CKB1, CKB2	CKA2	7, 56, 116, 139, 142, 217, 373, 374, 379, 405
YAK1	Serine-threonine protein kinase; component of a glucose-sensing system that inhibits growth in response to glucose availability; upon nutrient deprivation Yak1p phosphorylates Pop2p to regulate mRNA	S38; T288; Y530	Y530	YAK1		7, 13, 122, 142, 152, 175, 217, 374, 379

	deadenylation, the co-repressor Crf1p to inhibit transcription of ribosomal genes, and the stress-responsive transcription factors Hsf1p and Msn2p; nuclear localization negatively regulated by the Ras/PKA signaling pathway in the presence of glucose				
NSP1	FG-nucleoporin component of central core of the nuclear pore complex; also part of the nuclear pore complex (NPC) nuclear basket; contributes directly to nucleocytoplasmic transport and maintenance of the NPC permeability barrier; found in stable complex with Nup82p, Gle2p and two other FG-nucleoporins (Nup159p and Nup116p); also found in stable complex with Nic96p and two other FG-nucleoproteins (Nup49p and Nup57p)		S361	RAD53	7, 370, 379
CYC8	General transcriptional co-repressor; acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters; can form the prion [OCT+]	S421; T426; S429; S741; S768; S815; S817; S943	S780	MEC1, TEL1	7, 370
			S815	KNS1	7, 32, 142, 217, 370, 374, 379
			S819	KNS1	32, 142, 379
ABP1	Actin-binding protein of the cortical actin cytoskeleton; important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; inhibits barbed-end actin filament elongation; phosphorylation within its Proline-Rich Regio, mediated by Cdc28p and Pho85p, protects Abp1p from proteolysis mediated by its own PEST sequences; mammalian homolog of HIP-55 (hematopoietic progenitor kinase 1 [HPK1]-interacting protein of 55 kDa)	T157; S163; T165; S167; S169; S174; T181; S183; S313; S475; S478; S481	S26	PTK2	32

			S169	CDC28, CLB2		7, 32, 56, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S183	CDC28		7, 32, 56, 100, 116, 142, 152, 217, 370, 373, 374, 379
			S313	CDC28		7, 32, 116, 142, 373, 379
			T30	PTK2		32
			T31	PTK2		32
			T165	CDC28, CLB2	PHO85	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			T181	CDC28, CLB2	PHO85	7, 32, 56, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
HSP26	Small heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation; long-lived protein that is preferentially retained in mother cells and forms cytoplasmic foci; oligomer activation requires heat-induced conformational change; also has mRNA binding activity	S2; S5; T42; S47; T48; S208; S211	S208	MEC1, TEL1		7, 52, 100, 142, 152, 379
			S211	MEC1, TEL1		7, 52, 100, 122, 139,

							142, 152, 374, 379
VMA2	Subunit B of V1 peripheral membrane domain of vacuolar H+-ATPase; electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the cytoplasm; protein abundance increases in response to DNA replication stress; human homolog ATP6V1B1, implicated in autosomal-recessive distal renal tubular acidosis (RTA) with sensorineural deafness, complements yeast null mutant	T501; S503; S504; S511; S515	S503	SNF1			7, 32, 56, 370, 374
			S511	MEC1, TEL1	CKA2		7, 116, 139, 142, 152, 217, 370, 373, 374, 379
PDA1	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex; catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA; phosphorylated; regulated by glucose; PDH complex is concentrated in spots within the mitochondrial matrix, often near the ERMES complex and near peroxisomes	Y309; S313; S315	S313	PKP1, PKP2	CKA2		7, 32, 56, 100, 110, 122, 139, 142, 152, 217, 258, 331, 370, 374, 379
OM45	Mitochondrial outer membrane protein of unknown function; major constituent of the outer membrane, extending into the intermembrane space; interacts with porin (Por1p) and with Om14p; imported via the presequence pathway involving the TOM and TIM23 complexes, then assembled in the outer membrane by Mim1p; protein abundance increases in response to DNA replication stress	T207	T207		SNF1	PPH22	7, 32, 139, 379
APA1	AP4A phosphorylase; bifunctional diadenosine 5',5'''-P1,P4-tetraphosphate phosphorylase and ADP sulfurylase involved in catabolism of bis(5'-	T60; T75	T60	KNS1			7, 32, 142, 217, 370, 379

	nucleosidyl) tetraphosphates; catalyzes phosphorolysis of dinucleoside oligophosphates, cleaving substrates' alpha/beta-anhydride bond and introducing Pi into the beta-position of the corresponding NDP formed; protein abundance increases under DNA replication stress; APA1 has a paralog, APA2, that arose from the whole genome duplication					
PFK1	Alpha subunit of heterooctameric phosphofructokinase; involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes	S166; S179; S188; S189; S192	S3	MEC1, TEL1	CKA2	7, 52, 139, 379
PFK2	Beta subunit of heterooctameric phosphofructokinase; involved in glycolysis; indispensable for anaerobic growth; activated by fructose-2,6-bisphosphate and AMP; mutation inhibits glucose induction of cell cycle-related genes	S36; S41; S42; S47; T48; S148; T149; T152; S160; S163; S166; S167; S171; Y172; T173; Y177	S166	SNF1		7, 32, 116, 142, 152, 217, 370, 373, 379
			S167	SNF1		7, 32, 116, 142, 152, 217, 370, 373, 379
			S171	SNF1	CKA2	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S652	PKC1		81
			Y172	SNF1		7, 32, 139
SEC2	Guanyl-nucleotide exchange factor for the small G-protein Sec4p; essential for post-Golgi vesicle transport and for autophagy;	S632; S740	S515	SNF1	CKA2	7, 32, 116, 139, 142, 152, 217,

	associates with the exocyst, via exocyst subunit Sec15p, on secretory vesicles				373, 374, 379
SAC7	GTPase activating protein (GAP) for Rho1p; regulator of a Tor2p-mediated, Rho1p GTPase switch that controls organization of the actin cytoskeleton; negative regulator of the RHO1-PKC1-MAPK cell integrity (CWI) and membrane fluidity homeostasis signaling pathways; potential Cdc28p substrate; SAC7 has a paralog, BAG7, that arose from the whole genome duplication		S16	CDC28	32, 142, 374, 379
			S46	CDC28, CLB2	56, 142, 217, 379
PHO81	Cyclin-dependent kinase (CDK) inhibitor; regulates Pho80p-Pho85p and Pcl7p-Pho85p cyclin-CDK complexes in response to phosphate levels; inhibitory activity for Pho80p-Pho85p requires myo-D-inositol heptakisphosphate (IP7) generated by Vip1p; relative distribution to the nucleus increases upon DNA replication stress	S542; S543	S956	RAD53	7, 52
STE4	G protein beta subunit; forms a dimer with Ste18p to activate mating signaling pathway, forms heterotrimer with Gpa1p and Ste18p to dampen signaling; pheromone-induced phosphorylation plays critical role in chemotropism; may recruit Rho1p to polarized growth site during mating; contains WD40 repeats		S335	FUS3	216, 379
			T320	FUS3	216, 379
FPR1	Peptidyl-prolyl cis-trans isomerase (PPIase); binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; N-terminally propionylated in vivo; mutation is functionally complemented by human FKBP1A	S45; S46; S51	S51	PSK2	7, 32, 142, 370, 379

SUI2	Alpha subunit of the translation initiation factor eIF2; eIF2 is involved in identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; protein abundance increases in response to DNA replication stress	S292; S294; S301	S52	GCN2	76, 374, 387, 411, 459
			S292	CKA1, CKA2, CKB1, CKB2	7, 98, 100, 116, 142, 152, 373, 374, 379, 411
			S294	CKA1, CKA2, CKB1, CKB2	7, 98, 100, 116, 142, 152, 373, 374, 379, 411
			S301	CKA1, CKA2, CKB1, CKB2	7, 98, 100, 116, 142, 152, 373, 374, 379, 411
NUP1	FG-nucleoporin component of central core of the nuclear pore complex; contributes directly to nucleocytoplasmic transport and maintenance of thenuclear pore complex (NPC) permeability barrier; possible karyopherin release factor that accelerates release of karyopherin-cargo complexes after transport across NPC; both NUP1 and NUP60 are homologous to human NUP153	T769; S770; S796	S161	CDC28	38, 116, 142, 217, 329, 373, 379
			S383	RAD53	7, 370
			S449	RAD53	370
			S592	RAD53	7, 370
			S615	RAD53	370
			S637	RAD53	7, 370, 379
			S656	RAD53	7, 52, 370
			S672	RAD53	370
			S754	RAD53	7, 370

			S767	RAD53	7, 142, 217, 379
			T344	CDC28	38
MCK1	Dual-specificity ser/thr and tyrosine protein kinase; roles in chromosome segregation, meiotic entry, genome stability, phosphorylation-dependent protein degradation (Rcn1p and Cdc6p), inhibition of protein kinase A, transcriptional regulation, inhibition of RNA pol III, calcium stress and inhibition of Clb2p-Cdc28p after nuclear division; MCK1 has a paralog, YGK3, that arose from the whole genome duplication	S24; S27; T30; S196; S198; Y199; S202	Y199	MCK1	7, 32, 142, 152, 217, 328, 374, 379
NPR1	Protein kinase; stabilizes several plasma membrane amino acid transporters by antagonizing their ubiquitin-mediated degradation; phosphorylates Aly2p; negatively regulates Ldb19p-mediated endocytosis through phosphorylation of Ldb19p, which prevents its association with the plasma membrane; Npr1p activity is negatively regulated via phosphorylation by the TOR complex; NPR1 has a paralog, PRR2, that arose from the whole genome duplication	S45; S46; S47; S51	S47	NPR1	105, 142, 374, 379
			S85	TOR1	105
			S90	TOR1	105
			S100	TOR1	7, 105
			S111	TOR1	105
			S116	TOR1	7, 105
			S125	TOR1	105, 142, 217, 379
			S137	TOR1	105, 142, 379
			S141	TOR1	105, 142, 379
			S159	TOR1	105, 142, 370, 379

			S255	TOR1	7, 105, 217, 374
			S257	NPR1	105, 142, 217, 374
			S259	TOR1	105, 142
			S260	TOR1	105, 142, 217, 374, 379
			S288	TOR1	105
			S292	TOR1	105
			S317	TOR1	100, 105, 142, 217, 379
			S320	TOR1	105, 379
			S328	TOR1	105
			S336	TOR1	105
			S338	TOR1	37, 105, 142
			S339	TOR1	105, 142
			S347	TOR1	37, 105
			S349	TOR1	105
			S353	TOR1	32, 105, 142, 217, 374
			S356	TOR1	7, 32, 37, 105, 142, 217, 374
			S357	NPR1	7, 32, 37, 105, 142, 217, 374, 379
			S385	TOR1	105
SIN3	Component of both the Rpd3S and Rpd3L histone deacetylase complexes; involved in transcriptional repression and activation of diverse processes, including mating-type switching and meiosis; involved in the maintenance of chromosomal integrity	T303; T304; T308	S316	CDC28	7, 32, 100, 142, 217, 374, 379
			S1126	MEC1, TEL1	52

			T304	CDC28			7, 32, 142, 217, 374, 379
HSP12	Plasma membrane protein involved in maintaining membrane organization; involved in maintaining organization during stress conditions; induced by heat shock, oxidative stress, osmostress, stationary phase, glucose depletion, oleate and alcohol; protein abundance increased in response to DNA replication stress and dietary restriction; regulated by the HOG and Ras-Pka pathways; required for dietary restriction-induced lifespan extension		S21	MEC1, TEL1		PTC6	7, 32, 52, 56, 116, 142, 370, 373, 379
			S24	PKP1		PTC6	7, 32, 56, 116, 142, 370, 373, 379
			S59	PKP1			7, 32, 116, 142, 370, 373, 379
			S73	PKP1			7, 32, 116, 139, 142, 370, 373, 379
			S87	PKP1			7, 32, 370
			Y25	PKP1			32, 142
TAF2	TFIID subunit (150 kDa); involved in RNA polymerase II transcription initiation	S318	T19				7, 142, 370
GSY1	Glycogen synthase; expression induced by glucose limitation, nitrogen starvation, environmental stress, and entry into stationary phase; GSY1 has a paralog, GSY2, that arose from the whole genome duplication; relocalizes from nucleus to cytoplasmic foci upon DNA replication stress	S651; S655	S651	MCK1	RIM11		7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S655	MCK1	PHO85		7, 32, 56, 100, 116, 122, 139,

						142, 152, 217, 370, 373, 374, 379
STE11	Signal transducing MEK kinase; involved in pheromone response and pseudohyphal/invasive growth pathways where it phosphorylates Ste7p, and the high osmolarity response pathway, via phosphorylation of Pbs2p; regulated by Ste20p and Ste50p; protein abundance increases in response to DNA replication stress		S281	STE20		86
			S285	STE20		86
			T286	STE20		86
SSD1	Translational repressor with a role in polar growth and wall integrity; regulated by Cbk1p phosphorylation to effect bud-specific translational control and localization of specific mRNAs; interacts with TOR pathway components; contains a functional N-terminal nuclear localization sequence and nucleocytoplasmic shuttling appears to be critical to Ssd1p function	S480; S481; T482; S487; S489; S491; S492; T494	S42	CBK1		156, 217
			S126	CBK1		32, 142, 152, 156
			S152	CBK1		32, 142, 156, 374, 379
			S164	CBK1		32, 56, 142, 156, 217, 370, 374
			S228	CBK1		32, 142, 156
			S231	CDC28		7, 32, 142, 156, 370
			S267	CLB2, CDC28	CDC28	7, 32, 139, 142, 152
			S286	CDC28		7, 32, 142, 152, 156, 374, 379
			S293	CKB1		32, 142, 156

			S319	CKB1		156
			S492	CDC28		7, 32, 100, 116, 142, 217, 370, 373, 374, 379
			T261	CBK1		156
UBP1	Ubiquitin-specific protease; removes ubiquitin from ubiquitinated proteins; cleaves at the C terminus of ubiquitin fusions irrespective of their size; capable of cleaving polyubiquitin chains	S555; S638; S755	S530	CKA1	CKA2	7, 32, 100, 116, 139, 142, 152, 217, 373, 379
			S531	CKA1	CKA2	7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 379
NAP1	Histone chaperone; involved in histone exchange by removing and replacing histone H2A-H2B dimers or histone variant dimers from assembled nucleosomes; involved in the transport of H2A and H2B histones to the nucleus; required for the regulation of microtubule dynamics during mitosis; interacts with mitotic cyclin Clb2p; controls bud morphogenesis; phosphorylated by CK2; protein abundance increases in response to DNA replication stress	T20; T24	S159	CKA1, CKA2, CKB1, CKB2		7, 32, 37, 43, 116, 139, 142, 152, 217, 370, 373
			S177	CKA1, CKA2, CKB1, CKB2	CKA2	7, 32, 37, 43, 116, 139, 142, 152, 217, 370, 373, 379
			S397	CKA1, CKA2, CKB1, CKB2		7, 43
			T20	PTK2		7, 32, 37, 116, 122,

						142, 152, 217, 370, 373, 374, 379
			T24	PTK2		7, 32, 37, 116, 122, 142, 152, 217, 373, 374, 379
FEN1; ELO2	Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; ELO2 has a paralog, ELO1, that arose from the whole genome duplication; lethality of the elo2 elo3 double null mutation is functionally complemented by human ELOVL1 and weakly complemented by human ELOVL3 or ELOV7	T334; S336; S338	S336	MCK1	PHO85	7, 32, 56, 100, 139, 142, 152, 217, 370, 374, 379
			S338	MCK1		7, 32, 56, 100, 142, 152, 217, 370, 374, 379
			T334	MCK1	PHO85	7, 32, 56, 100, 139, 142, 152, 217, 370, 374, 379
USO1	Essential protein involved in vesicle-mediated ER to Golgi transport; binds membranes and functions during vesicle docking to the Golgi; required for assembly of the ER-to-Golgi SNARE complex		S1032	RAD53		7, 370, 379
RPC53	RNA polymerase III subunit C53	S119; S224; T228; T232; S234	S224	MCK1		7, 32, 56, 116, 142, 152, 204, 217, 370,

							373, 374, 379
			T228	MCK1			32, 56, 116, 122, 142, 152, 204, 217, 370, 373, 374, 379
			T232	MCK1			7, 32, 56, 116, 122, 142, 152, 204, 217, 373, 374, 379
HSP30	Negative regulator of the H(+)-ATPase Pma1p; stress-responsive protein; hydrophobic plasma membrane localized; induced by heat shock, ethanol treatment, weak organic acid, glucose limitation, and entry into stationary phase	S308; T331	S308		CDC28	SIT4	7, 32, 100, 139, 142, 370, 379
PWP2	Conserved 90S pre-ribosomal component; essential for proper endonucleolytic cleavage of the 35 S rRNA precursor at A0, A1, and A2 sites; contains eight WD-repeats; PWP2 deletion leads to defects in cell cycle and bud morphogenesis	S232	S664	MEC1, TEL1			7, 52, 142
CDC48	AAA ATPase; subunit of polyUb-selective segregase complex involved in ERAD, INM-associated degradation (INMAD), mitotic spindle disassembly, macroautophagy, PMN, ribosome-associated degradation, ribophagy, homotypic ER membrane fusion, SCF complex disassembly, cell wall integrity during heat stress, and telomerase regulation; mobilizes membrane-anchored transcription factors by regulated Ub/proteasome-dependent processing (RUP); human ortholog VCP complements a cdc48 mutant	S770	S770	MPS1			7, 32, 37, 56, 116, 142, 217, 370, 373, 374, 379

			T735	MPS1	CKA2		7, 37, 139, 142, 370, 379
PPZ1	Serine/threonine protein phosphatase Z, isoform of Ppz2p; involved in regulation of potassium transport, which affects osmotic stability, cell cycle progression, and halotolerance		S49			OCA1	32, 142, 217, 379
			S142	CDC28			142, 379
			S265	CLB2, CDC28			142, 217, 379
			T261	CLB2, CDC28			142, 217, 379
CDC60	Cytosolic leucyl tRNA synthetase; ligates leucine to the appropriate tRNA; human homolog LARS can complement yeast temperature-sensitive mutant at restrictive temperature	T142; T152	T142	CDC28			116, 142, 373
RFA2	Subunit of heterotrimeric Replication Protein A (RPA); RPA is a highly conserved single-stranded DNA binding protein involved in DNA replication, repair, and recombination; RPA protects against inappropriate telomere recombination, and upon telomere uncapping, prevents cell proliferation by a checkpoint-independent pathway; in concert with Sgs1p-Top2p-Rmi1p, stimulates DNA catenation/decatenation activity of Top3p; protein abundance increases in response to DNA replication s		S27	IME2			7, 62, 345
			S122	IME2			7, 25, 52, 56, 113, 116, 122, 139, 142, 217, 373, 374, 379
GSY2	Glycogen synthase; expression induced by glucose limitation, nitrogen starvation, heat shock, and stationary phase; activity	S651; S655	S651	MCK1	RIM11		7, 32, 37, 100, 122, 133, 139,

	regulated by cAMP-dependent, Snf1p and Pho85p kinases as well as by the Gac1p-Glc7p phosphatase; GSY2 has a paralog, GSY1, that arose from the whole genome duplication; relocalizes from cytoplasm to plasma membrane upon DNA replication stress				142, 148, 149, 152, 217, 342, 370, 374, 379, 427
			S655	PCL10, PHO85	7, 26, 37, 100, 122, 133, 142, 148, 149, 217, 342, 370, 374, 379, 427
			T668	PCL10, PHO85	26, 133, 148, 149, 427
SPT5	Spt4p/5p (DSIF) transcription elongation factor complex subunit; the Spt4/5 complex binds to ssRNA in a sequence-specific manner, and in concert with RNAP I and II has multiple roles regulating transcriptional elongation, RNA processing, quality control, and transcription-coupled repair; interacts with DNA upstream of RNAPII and the non-template strand of the transcription bubble; Spt5p is the only transcription elongation factor conserved in all domains of life	T40	S931	BUR2, SGV1	227
			S937	BUR2, SGV1	227
			S948	BUR2, SGV1	227
			S958	BUR2, SGV1	227
			S969	BUR2, SGV1	227
			S975	BUR2, SGV1	227
			S981	BUR2, SGV1	227

			S987	BUR2, SGV1	227
			S1000	BUR2, SGV1	227
			S1009	BUR2, SGV1	227, 379
			S1015	BUR2, SGV1	142, 227, 379
			S1032	BUR2, SGV1	142, 152, 227, 379
			S1043	BUR2, SGV1	152, 227, 379
			S1052	BUR2, SGV1	142, 227, 379
			S1058	BUR2, SGV1	152, 227, 379
MIG1	Transcription factor involved in glucose repression; sequence specific DNA binding protein containing two Cys2His2 zinc finger motifs; regulated by the SNF1 kinase and the GLC7 phosphatase; regulates filamentous growth along with Mig2p in response to glucose depletion; activated in stochastic pulses of nuclear localization, shuttling between cytosol and nucleus depending on external glucose levels and its phosphorylation state	S278	S222	SNF1	32, 77, 142, 152, 367, 428
			S264	CLB2, CDC28	32, 142, 152, 379
			S278	SNF1	7, 32, 77, 142, 152, 299, 367, 379, 396, 428
			S311	SNF1	6, 7, 77, 122, 142, 152, 217, 299, 307, 370, 379, 396, 428

			S381	SNF1		7, 77, 142, 367, 428
FUN19	Non-essential protein of unknown function; expression induced in response to heat stress; FUN19 has a paralog, YOR338W, that arose from the whole genome duplication	T194; S207; S267; S269	S207	CDC28	PHO85	7, 139, 142
			S211	CDC28		7, 142
GAC1	Regulatory subunit for Glc7p type-1 protein phosphatase (PP1); tethers Glc7p to Gsy2p glycogen synthase, binds Hsf1p heat shock transcription factor, required for induction of some HSF-regulated genes under heat shock; GAC1 has a paralog, PIG1, that arose from the whole genome duplication		S66	CLB2, CDC28		142, 379
HRR25	Conserved casein kinase; regulates diverse events including: vesicular traffic, DNA repair, the CVT pathway, monopolar attachment of sister kinetochores at meiosis I, and ribosomal subunit biogenesis; monopolin subunit; binds the RNAPII CTD; phosphorylates COPII coat subunits; interacts with Sit4p phosphatase; antagonizes calcineurin signaling, reducing nuclear accumulation of Crz1p; phosphorylates Dsn1p, the kinetochore receptor for monopolin; homolog of mammalian CK1delta	S325; T326; S330; T332	S330	MPS1		37, 116, 142, 217, 370, 373, 374, 379
BMH1	14-3-3 protein, major isoform; controls proteome at post-transcriptional level, binds proteins and DNA, involved in regulation of exocytosis, vesicle transport, Ras/MAPK and rapamycin-sensitive signaling, aggresome formation, spindle position checkpoint; protein increases in abundance and relative distribution to the nucleus increases upon DNA replication stress; antiapoptotic gene similar to human 14-3-3; BMH1 has a paralog, BMH2, that arose from whole genome duplication	T231; T234; S235; S238; S240	S238	HRR25		32, 63, 142, 374, 417

BEM1	Protein containing SH3-domains; involved in establishing cell polarity and morphogenesis; functions as a scaffold protein for complexes that include Cdc24p, Ste5p, Ste20p, and Rsr1p	S458	S72			7, 32, 131, 370, 379, 401
			S458		SNF1	7, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
MCM2	Protein involved in DNA replication; component of the Mcm2-7 hexameric helicase complex that binds chromatin as a part of the pre-replicative complex; relative distribution to the nucleus increases upon DNA replication stress	T547	S107	CDC7		323
			S164	CDC7		39, 142, 310, 311, 323, 376
			S170	CDC7		39, 142, 310, 311, 323, 376
ZIP1	Transverse filament protein of the synaptonemal complex; required for normal levels of meiotic recombination and pairing between homologous chromosome during meiosis; required for meiotic recombination between non-allelc sites; potential Cdc28p substrate		S75	Kinase MEC1	PPH3, PSY2	94
			S89	CLB5, CDC28		460
			S763	CLB5, CDC28		379, 460
			S783	CLB5, CDC28		379, 460
			S828	CLB5, CDC28		460
NTH1	Neutral trehalase, degrades trehalose; required for thermotolerance and may	S83	S20	TPK1		7, 100, 104, 122, 142,

	mediate resistance to other cellular stresses; phosphorylated and activated by Cdc28p at the G1/S phase transition to coordinately regulate carbohydrate metabolism and the cell cycle; inhibited by Dcs1p; NTH1 has a paralog, NTH2, that arose from the whole genome duplication				217, 370, 379, 423
			S66	CDC28	7, 32, 56, 100, 104, 142, 152, 370, 374, 379, 423
			S83	TPK1	7, 32, 56, 100, 104, 142, 152, 370, 374, 379, 423
PUP2	Alpha 5 subunit of the 20S proteasome; involved in ubiquitin-dependent catabolism; human homolog is subunit zeta	T55; S56; S251	S56	CDC28	7, 122, 142, 181, 217, 370, 374, 379
CDC3	Component of the septin ring that is required for cytokinesis; septins are GTP-binding proteins that assemble with other septins into rod-like complexes that can associate with other rods to form filament polymers; septin rings at the mother-bud neck act as scaffolds for recruiting factors needed for cell division and as barriers to prevent diffusion of specific proteins between mother and daughter cells	S2; S9	S498	CTK1	32, 379
			S503	CLB2, CDC28	32, 116, 122, 142, 152, 373, 374, 379, 389
			S509	CLB2, CDC28	7, 32, 37, 116, 142, 152, 217, 373, 374, 379, 389

HOG1	Mitogen-activated protein kinase involved in osmoregulation; controls global reallocation of RNAPII during osmotic shock; mediates recruitment/activation of RNAPII at Hot1p-dependent promoters; binds calmodulin; stimulates antisense transcription to activate CDC28; defines novel S-phase checkpoint with Mrc1p that prevent replication/transcription conflicts; nuclear form represses pseudohyphal growth; autophosphorylates; protein abundance increases under DNA replication stress	Y176; T179	T174	PBS2	PTC2, PTC3	18, 30, 32, 37, 100, 152, 241, 352, 379, 408, 420
			Y176	PBS2	PTC1	7, 18, 30, 32, 100, 139, 142, 152, 241, 352, 379, 408, 420
NIP1	eIF3c subunit of the eukaryotic translation initiation factor 3 (eIF3); involved in the assembly of preinitiation complex and start codon selection; eIF3 is also involved in programmed stop codon readthrough	S98; S99; S103; S222; T228; T239	S98	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
			S99	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
			S103	TEL1		7, 32, 96, 100, 142, 152, 217, 370, 374, 379
NUP2	Nucleoporin involved in nucleocytoplasmic transport; binds to either the nucleoplasmic or cytoplasmic faces of the nuclear pore complex depending on Ran-GTP levels; also has a role in chromatin organization	T14; S17; S20; S84; S203; S205; S537; S538; S540; T577; S581	S17	MCK1		7, 32, 56, 100, 116, 142, 152, 217, 369, 373, 374, 379

		S20	MCK1		7, 32, 56, 100, 116, 142, 152, 217, 369, 373, 374, 379
		S68	RAD53		7, 139, 142, 370
		S203	RAD53	PTP1	7, 32, 56, 116, 142, 152, 217, 370, 373, 374
		S205	ALK2	PTP1	7, 32, 56, 116, 142, 152, 217, 370, 373, 374
		S248	RAD53		7, 370
		S284	RAD53		7, 370
		S317	RAD53		7, 370
		S351	RAD53		7, 52, 370
		S368	RAD53		7, 142, 370, 379
		S399	MEC1, TEL1		370, 379
		S512	RAD53		370
		S523	RAD53		370
NAB2	Nuclear polyadenylated RNA-binding protein; required for nuclear mRNA export and poly(A) tail length control; stimulates RNA polymerase III transcription by enhancing TFIIIB binding to promoters; protects mRNA against decay by the nuclear exosome in a poly(A)-tail-dependent manner; involved in forming export-competent mRNPs in the nucleus; autoregulates mRNA levels; NLS binds Kap104p; protein abundance increases	S180	SLT2		45

	under DNA replication stress; related to human hnRNPs				
			T178	SLT2	45
PAN1	Part of actin cytoskeleton-regulatory complex Pan1p-Sla1p-End3p; associates with actin patches on cell cortex; promotes protein-protein interactions essential for endocytosis; binds to and activates Arp2/3 complex in vitro; phosphorylation of Thr-1225 is regulated by MAPK Hog1p in response to osmotic stress; previously thought to be a subunit of poly(A) ribonuclease	T570; T993; S1003; S1250; S1253; S1255; T1256	T148	PRK1	147, 395, 453
			T170	PRK1	147, 395, 453
			T194	PRK1	147, 395, 453
			T221	PRK1	395, 453
			T241	PRK1	7, 147, 395, 453
			T398	PRK1	147, 395, 453
			T415	PRK1	147, 395, 453
			T428	PRK1	147, 395, 453
			T452	PRK1	147, 395, 453
			T473	PRK1	147, 395, 453
			T504	PRK1	147, 395, 453
			T513	PRK1	147, 395, 453
			T544	PRK1	147, 395, 453
			T551	PRK1	147, 395, 453
			T566	PRK1	7, 146

			T570	PRK1		7, 32, 142, 147, 152, 379, 395, 453
PAH1	Mg2+-dependent phosphatidate (PA) phosphatase; dephosphorylates PA to yield diacylglycerol; regulates phospholipid synthesis, nuclear/ER membrane growth, lipid droplet formation, triacylglycerol synthesis, vacuolar homeostasis and cell wall integrity; phosphorylated by Pho85p/Pho80p, Cdc28p/Cyclin B, PKA, PKC, and CKII, regulating activity, localization, and proteosomal degradation; homolog of mammalian lipins 1 and 2; human homologs LPIN1, LPIN2, LPIN3 complement the null	T163; T164; S166; T170; T175; T176; S814	S110		NEM1, SPO7	58, 60, 289
			S114		NEM1, SPO7	58, 60, 289
			S168		NEM1, SPO7	58, 60, 116, 289, 373, 379
			S602	CDC28	NEM1, SPO7	7, 58, 60, 142, 217, 289, 379
			S744		NEM1, SPO7	7, 58, 60, 116, 142, 152, 217, 289, 373, 374, 379
			S748		NEM1, SPO7	7, 58, 60, 116, 122, 142, 152, 217, 289, 373, 374, 379
			T723		NEM1, SPO7	58, 60, 289
SIP1	Alternate beta-subunit of the Snf1p kinase complex; may confer substrate specificity; vacuolar protein containing KIS (Kinase-Interacting Sequence) and ASC	S331	S198	CDC28		142, 217, 379

	(Association with Snf1 kinase Complex) domains involved in protein interactions					
			S200	CDC28		7, 116, 142, 217, 373, 374, 379
SRP40	Nucleolar serine-rich protein; role in preribosome assembly or transport; may function as a chaperone of small nucleolar ribonucleoprotein particles (snoRNPs); immunologically and structurally to rat Nopp140	S133; T141	S133		SIW14	32, 56, 116, 152, 373
STH1	ATPase component of the RSC chromatin remodeling complex; required for expression of early meiotic genes; promotes base excision repair in chromatin; essential helicase-related protein homologous to Snf2p	S51; S52; S1188	S1172	MEC1, TEL1		52
			T1166	MEC1, TEL1		7, 52, 139
RAD23	Protein with ubiquitin-like N terminus; subunit of Nuclear Excision Repair Factor 2 (NEF2) with Rad4p that binds damaged DNA; enhances protein deglycosylation activity of Png1p; also involved, with Rad4p, in ubiquitylated protein turnover; Rad4p-Rad23p heterodimer binds to promoters of DNA damage response genes to repress their transcription in the absence of DNA damage	S104; T107; S110	S121	MEC1, TEL1		7, 32, 52, 379
SLA1	Cytoskeletal protein binding protein; required for assembly of the cortical actin cytoskeleton; interacts with proteins regulating actin dynamics and proteins required for endocytosis; found in the nucleus and cell cortex; has 3 SH3 domains	S794; T797; S799; T831; T834; T835	S437	CLB2, CDC28		7, 32, 142, 152, 370, 374, 379
			S449		PSR2	7, 32, 116, 142, 217, 373, 379

YSC84	Actin-binding protein; involved in bundling of actin filaments and endocytosis of actin cortical patches; activity stimulated by Las17p; contains SH3 domain similar to Rvs167p; YSC84 has a paralog, LSB3, that arose from the whole genome duplication	Y296; S301	S311			7, 32, 142, 217, 374, 379
UGP1	UDP-glucose pyrophosphorylase (UGPase); catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; involved in PKA-mediated oxidative stress resistance and long-term survival in stationary phase; UGP1 has a paralog, YHL012W, that arose from the whole genome duplication		S11	PSK2		7, 32, 37, 56, 100, 116, 122, 142, 217, 342, 368, 373, 374, 379
CBF5	Pseudouridine synthase catalytic subunit of box H/ACA snoRNPs; acts on large and small rRNAs, on snRNA U2, and on some mRNAs; mutations in human ortholog dyskerin cause the disorder dyskeratosis congenita; small nucleolar ribonucleoprotein particles are also known as snoRNPs	T378; S398	S395	MEC1, TEL1	RIM11	7, 32, 52, 116, 139, 142, 373, 374, 379
			S399	MEC1, TEL1		7, 32, 52, 116, 142, 370, 373, 374, 379
			T396	FRK1	CKA2	7, 32, 139, 142
PPZ2	Serine/threonine protein phosphatase Z, isoform of Ppz1p; involved in regulation of potassium transport, which affects osmotic stability, cell cycle progression, and halotolerance	T298; S299; S310; S314; S315; S317; S359; S362	S299	CLB2, CDC28		7, 37, 142, 374, 379
			S310	CLB2, CDC28		7, 37, 116, 142, 373, 374, 379
SLA2	Adaptor protein that links actin to clathrin and endocytosis; involved in membrane		S308	CDC28		7, 32, 100, 142, 152,

	cytoskeleton assembly and cell polarization; present in the actin cortical patch of the emerging bud tip; dimer in vivo					217, 374, 379
			T290	SSK2		7, 32, 142, 217, 370, 374, 379
			T294	CDC28		7, 32, 100, 122, 142, 217, 370, 374, 379
			T296	CDC28		7, 32, 100, 122, 142, 217, 370, 374, 379
			T298	CDC28		7, 32, 100, 142, 152, 217, 370, 374, 379
PGM1	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; PGM1 has a paralog, PGM2, that arose from the whole genome duplication	T111; T118; S120; S513	S120	FRK1		7, 32, 116, 122, 142, 152, 217, 370, 373, 374, 379
TRM2	tRNA methyltransferase; 5-methylates the uridine residue at position 54 of tRNAs and may also have a role in tRNA stabilization or maturation; endo-exonuclease with a role in DNA repair	S93	S92	KNS1	CLA4	7, 32, 56, 116, 139, 142, 152, 217, 370, 373, 374, 379
			S93	KNS1		7, 32, 56, 142, 152, 217, 370, 374, 379
MKS1	Pleiotropic negative transcriptional regulator; involved in Ras-CAMP and lysine biosynthetic pathways and nitrogen regulation; involved in retrograde (RTG) mitochondria-to-nucleus signaling	S440; S442	S217	FRK1		7, 32, 139

TGL1	Steryl ester hydrolase; one of three gene products (Yeh1p, Yeh2p, Tgl1p) responsible for steryl ester hydrolase activity and involved in sterol homeostasis; localized to lipid particle membranes	S462; S466; S538	S466	CDC28		142, 379
			S492	TPK3		7, 32, 142, 370, 374, 379
EDE1	Scaffold protein involved in the formation of early endocytic sites; putative regulator of cytokinesis; homo-oligomerization is required for localization to and organization of endocytic sites; has a network of interactions with other endocytic proteins; binds membranes in a ubiquitin-dependent manner; may also bind ubiquitinated membrane-associated proteins; interacts with Cmk2 and functions upstream of CMK2 in regulating non-apoptotic cell death; homolog of mammalian Eps15	S241; S931; S1006; S1008; S1011; S1012; T1065; S1093; S1095; S1096; S1100; S1104; T1160; T1178; S1179; S1181; S1187; T1307; S1309	S241		PTC4	7, 32, 100, 122, 142, 152, 217, 370, 374, 379
			S244		PTC4	7, 32, 100, 122, 142, 152, 217, 374, 379
			S249		PTC4	7, 32, 142, 152, 217, 374, 379
			S527		PSR2	32, 152, 370
			S1069		CMP2	7, 32, 142, 379
			S1096	FUS3		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			S1100	PHO85		7, 32, 56, 100, 116, 142, 152, 217, 370,

						373, 374, 379
			T238	CDC28		7, 142, 217, 379
			T1072		CMP2	7, 32, 142, 379
PIN4	Protein involved in G2/M phase progression and response to DNA damage; interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage	T512; S538; S541; S545; S653; S655	S466	CDC28		7, 32, 116, 122, 139, 142, 217, 373, 374, 379
			S541	CDC28		32, 122, 142, 152, 379
			S653		SIT4	7, 32, 37, 116, 122, 142, 370, 373, 374, 379
			S655		SIT4	7, 32, 116, 122, 142, 370, 373, 374, 379
SHP1	UBX domain-containing substrate adaptor for Cdc48p; ubiquitin regulatory X domain-containing protein that acts as a substrate recruiting cofactor for Cdc48p; positively regulates Glc7p PPase activity to promote growth and mitotic progression in complex with Cdc48p; ubiquitinated protein interactor involved in ER-associated degradation (ERAD); regulated by nuclear Ub-dependent degradation (INMAD pathway) independent of the Asi and Doa10 complexes; homolog of human p47 (NSFL1C)	S97; S106; T107; S115; S224; S315; S321; S322; T331	S106	KNS1		7, 32, 100, 116, 152, 373, 379
			S108	PTK1		7, 32, 100, 116, 152,

						370, 373, 379
			S315	CDC28	CDC28	7, 32, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S322	CDC28		7, 32, 139, 142, 217, 374, 379
SCD5	Protein required for normal actin organization and endocytosis; targeting subunit for protein phosphatase type 1; undergoes Crm1p-dependent nuclear-cytoplasmic shuttling; multicopy suppressor of clathrin deficiency	S564; T568	T416	PRK1		146, 454
			T450	PRK1		146, 454
			T490	PRK1		7, 142, 146, 370, 454
TSA1	Thioredoxin peroxidase; acts as both ribosome-associated and free cytoplasmic antioxidant; self-associates to form high-molecular weight chaperone complex under oxidative stress; chaperone activity essential for growth in zinc deficiency; required for telomere length maintenance; binds and modulates Cdc19p activity; protein abundance increases, forms cytoplasmic foci during DNA replication stress; TSA1 has a paralog, TSA2, that arose from the whole genome duplication	T167; T174; T179; T183; S187	T174	FRK1		7, 32, 116, 142, 200, 373, 379
GCS1	ADP-ribosylation factor GTPase activating protein (ARF GAP); involved in ER-Golgi transport; required for prospore membrane formation; regulates phospholipase Spo14p; shares functional similarity with Glo3p; GCS1 has a paralog, SPS18, that arose from the whole genome duplication	S149; T151; S157; T161; S168; T170	S157	CKA1		7, 32, 142, 217, 370, 374, 379

			T151	MCK1		7, 32, 142, 152, 217, 370, 374
			T161	CDC28		7, 32, 139, 142, 217, 370, 374, 379
			T170	CLB2, CDC28		7, 32, 100, 142, 370, 379
DEF1	RNAPII degradation factor; forms a complex with Rad26p in chromatin, enables ubiquitination and proteolysis of RNAPII present in an elongation complex; mutant is deficient in Zip1p loading onto chromosomes during meiosis	T258; S260; S307	S273	RAD53		56, 116, 370
BDF1	Protein involved in transcription initiation; functions at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p; BDF1 has a paralog, BDF2, that arose from the whole genome duplication	S270; S612; S613; S615; T617	S630	MEC1, TEL1		52, 379
SWH1	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats and FFAT motif; interacts with ER anchor Scs2p at the nucleus-vacuole junction; regulated by sterol binding; SWH1 has a paralog, OSH2, that arose from the whole genome duplication	T432; S442; T443; S488; S490; S492; S678; S683; T694; S732; T1053; S1056	S1056	SNF1	SNF1	7, 32, 139, 142, 370, 379
			T1053	SNF1	SNF1	7, 32, 139, 370, 379
SIS2	Negative regulatory subunit of protein phosphatase 1 (Ppz1p); involved in coenzyme A biosynthesis; subunit of phosphopantothenoylcysteine decarboxylase (PPCDC: Cab3p, Sis2p, Vhs3p) complex and the CoA-Synthesizing Protein Complex (CoA-SPC: Cab2p, Cab3p, Cab4p, Cab5p,	T119; S121; S124; S130; S132	S47	CDC28		7, 32, 142, 217, 370, 374, 379

	Sis2p and Vhs3p); SIS2 has a paralog, VHS3, that arose from the whole genome duplication					
			S56	CDC28		7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
EAP1	eIF4E-associated protein, competes with eIF4G for binding to eIF4E; accelerates mRNA degradation by promoting decapping, facilitated by interaction with eIF4E; essential for Puf5p mediated repression; associates with Puf5p and Dhh1p; inhibits cap-dependent translation; functions independently of eIF4E to maintain genetic stability; plays a role in cell growth, implicated in the TOR signaling cascade	S389; S390; T391	S363		PSR1	32, 142
			S387	MCK1		7, 32
ELF1	Transcription elongation factor with a conserved zinc finger domain; implicated in the maintenance of proper chromatin structure in actively transcribed regions; deletion inhibits Brome mosaic virus (BMV) gene expression	S124; S142	S117	PSK2		7, 32, 116, 142, 193, 217, 370, 373, 374, 379
			S124	PSK2		7, 32, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
SPC42	Central plaque component of spindle pole body (SPB); involved in SPB duplication, may facilitate attachment of the SPB to the nuclear membrane	T357; T359	T357	MPS1		37, 142, 379
TTI1	Subunit of the ASTRA complex, involved in chromatin remodeling; telomere length regulator involved in the stability or	S817	S817		PPH22	7, 32, 116, 142, 370, 373, 374

	biogenesis of PIKKs such as TORC1; similar to S. pombe Tti1p; detected in highly purified mitochondria in high-throughput studies					
YKR018C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; protein abundance increases in response to DNA replication stress; YKR018C has a paralog, IML2, that arose from the whole genome duplication	T184; S185; S187; S192; T193; T196; T199; S246; S375; S377; S380	S380	PKH2		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
GPT2	Glycerol-3-phosphate/dihydroxyacetone phosphate sn-1 acyltransferase; located in lipid particles and the ER; involved in the stepwise acylation of glycerol-3-phosphate and dihydroxyacetone in lipid biosynthesis; the most conserved motifs and functionally relevant residues are oriented towards the ER lumen	S631; S632; S668; S671; T692; S693	T692	YPK1	CKA2	7, 32, 122, 139, 142, 370, 374, 379
PGM2	Phosphoglucomutase; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; functions as the acceptor for a Glc-phosphotransferase; protein abundance increases in response to DNA replication stress; PGM2 has a paralog, PGM1, that arose from the whole genome duplication	T111; T117; S119; S512	S119	RAD53		7, 32, 116, 122, 142, 370, 373, 374, 379
STV1	Subunit a of the vacuolar-ATPase V0 domain; one of two isoforms (Stv1p and Vph1p); Stv1p is located in V-ATPase complexes of the Golgi and endosomes while Vph1p is located in V-ATPase complexes of the vacuole	S223; S228	S223	CTK1		7, 32, 122, 142, 152, 217, 370, 374, 379
NOP4	Nucleolar protein; essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; constituent of 66S pre-ribosomal particles; contains four RNA recognition motifs (RRMs)	S247	S247			32, 142, 217, 374, 379

YRO2	Protein with a putative role in response to acid stress; null mutant is sensitive to acetic acid; transcription is regulated by Haa1p and induced in the presence of acetic acid; protein observed in plasma membrane foci in the presence of acetic acid; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies	T341; S343	S297		SIW14	32
			S299		SIW14	7, 32, 142, 370, 379
AKL1	Ser-Thr protein kinase; member (with Ark1p and Prk1p) of the Ark kinase family; involved in endocytosis and actin cytoskeleton organization	S407; S504; S541	S504	CLB2, CDC28		7, 32, 56, 139, 142, 152, 374, 379
			S801	CLB2, CDC28		7, 37, 116, 142, 217, 373, 379
			S1072	AKL1		7, 32, 34, 142, 152, 217, 338, 370, 374, 379
RTG3	bHLH/Zip transcription factor for retrograde (RTG) and TOR pathways; forms a complex with another bHLH/Zip protein, Rtg1p, to activate the pathways; target of Hog1p		S371		CMP2	32
ECM21	Protein involved in regulating endocytosis of plasma membrane proteins; identified as a substrate for ubiquitination by Rsp5p and deubiquitination by Ubp2p; promoter contains several Gcn4p binding elements; ECM21 has a paralog, CSR2, that arose from the whole genome duplication	S18; T20; S136; S140; S306; T959; S962; S1027; T1028; S1030	S33	CLB2, CDC28		32, 116, 142, 373, 379
			S550	DUN1		7, 52
			S1030	CDC28		7, 142, 152, 308, 379
			T1028	CDC28		7, 142, 152, 379

HEK2	RNA binding protein involved in asymmetric localization of ASH1 mRNA; represses translation of ASH1 mRNA, an effect reversed by Yck1p-dependent phosphoryation; regulates telomere position effect and length; similarity to hnRNP-K	S252; S358; S360; S362	S252		YVH1	7, 32, 301, 370, 374, 379
			S358	YCK1		7, 56, 142, 217, 301, 370, 374
			S360	YCK1		7, 142, 217, 301, 370, 374
			S362	YCK1		7, 142, 301, 370, 379
			S381	YCK1		7, 32, 139, 142, 301, 374
			T352	YCK1		301
			T355	YCK1		56, 142, 301, 374
NCL1	S-adenosyl-L-methionine-dependent tRNA: m5C-methyltransferase; methylates cytosine to m5C at several positions in tRNAs and intron-containing pre-tRNAs; increases proportion of tRNALeu(CAA) with m5C at wobble position in response to hydrogen peroxide, causing selective translation of mRNA from genes enriched in TTG codon; loss of NCL1 confers hypersensitivity to oxidative stress; similar to Nop2p and human proliferation associated nucleolar protein p120	T415; S423; S424; S431; T664; T665; S667; T671; T673; T675; S676; T677	S424	MKK2		7, 32, 116, 142, 373, 374, 379
			T426	CDC28		7, 32, 142, 379
IST2	Cortical ER protein involved in ER-plasma membrane tethering; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to the plasma membrane (PM) and regulate PM phosphatidylinositol-4-phosphate (PI4P)	T701; S704; T712; S714; T726; S729; Y730; T736; S757; S763; S764; S767;	S764	CTK1		32, 374

	levels by controlling access of Sac1p phosphatase to its substrate PI4P in the PM; localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process	S768; S844; S847; T850; T853			
			S767	YPK1	7, 32, 374, 379
SDS24	Protein involved in cell separation during budding; one of two S. cerevisiae homologs (Sds23p and Sds24p) of the S. pombe Sds23 protein, which is implicated in APC/cyclosome regulation; may play an indirect role in fluid-phase endocytosis; protein abundance increases in response to DNA replication stress; SDS24 has a paralog, SDS23, that arose from the whole genome duplication	T90; T92; S94; S98; S404; T441; S447; S458	S94	CTK1	7, 32, 56, 116, 142, 373, 379
			S458	CDC28	7, 142, 217, 370, 374, 379
TPS3	Regulatory subunit of trehalose-6-phosphate synthase/phosphatase; involved in synthesis of storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway; TPS3 has a paralog, TSL1, that arose from the whole genome duplication	S51; S52; T55; S56; S58; S59; Y61; S148; S150; S154; S181; S195	S148	CDC28	7, 32, 122, 142, 152, 217, 374, 379
TSL1	Large subunit of trehalose 6-phosphate synthase/phosphatase complex; Tps1p-Tps2p complex converts uridine-5'-diphosphoglucose and glucose 6-phosphate to trehalose; contributes to survival to acute lethal heat stress; mutant has aneuploidy tolerance; protein abundance increases in response to DNA replication stress; TSL1 has a paralog, TPS3, that arose from the whole genome duplication	S49; S53; S56; S71; S73; S77; S79; S85; S86; T87; T88; T115; S118; S135; S137; S138; S147; S155; S157; S161; S186; T191; S192; T194; S195; T205; T215;	S49	CKA1	7, 32, 122, 142, 379

		S216; T219; S220				
			S77	CDC28	CDC28	7, 32, 100, 122, 139, 142, 370, 374, 379
			S79	MCK1		7, 32, 142, 370
			S135	CDC28	CDC28	7, 32, 139, 142, 370, 374
			S147	CDC28	CDC28	7, 32, 139, 142, 370, 374, 379
			S155	MCK1		32, 142
			S157	MCK1		32
			S161	CDC28	CDC28	7, 32, 122, 139, 142, 374, 379
LEO1	Component of the Paf1 complex; which associates with RNA polymerase II and is involved in histone methylation; plays a role in regulating Ty1 transposition; involved in transcription elongation as demonstrated by the G-less-based run-on (GLRO) assay	S132; S358; S372; T374	S34	MEC1, TEL1		7, 142, 217, 370
			S132		CMP2	7, 32, 116, 142, 217, 373, 379
			S339	MEC1, TEL1		7, 32, 52, 139, 142, 217, 370, 374, 379
RFC1	Subunit of heteropentameric Replication factor C (RF-C); RF-C is a DNA binding protein and ATPase that acts as a clamp loader of the proliferating cell nuclear antigen (PCNA) processivity factor for DNA polymerases delta and epsilon	S40; S79; S80; T82; S88	T48	CLB2, CDC28		7, 142, 379

SIC1	Cyclin-dependent kinase inhibitor (CKI); inhibitor of Cdc28-Clb kinase complexes that controls G1/S phase transition, preventing premature S phase and ensuring genomic integrity; phosphorylated by Clb5/6-Cdk1 and Cln1/2-Cdk1 kinase which regulate timing of Sic1p degradation; phosphorylation targets Sic1p for SCF(CDC4)-dependent turnover; functional homolog of mammalian Kip1	S191	S69		33, 188, 262, 283, 287, 295, 414
			S76		33, 188, 261, 262, 283, 287, 295, 414, 441
			S80		37, 188, 262, 283, 414
			S145		37, 97, 122, 283, 295, 354, 414
			S191		7, 32, 37, 116, 122, 139, 142, 152, 272, 283, 373, 374, 414
			S201		7, 23, 37, 61, 64, 65, 116, 139, 142, 217, 374, 379
			T2	CDC28	33, 139, 283, 287, 295, 414
			T5		7, 139, 283, 287, 414
			T33		37, 97, 262, 283, 287, 354, 413, 414

			T45			37, 97, 262, 354, 379
			T48			33, 261, 262, 283, 295, 354, 414
			T173			7, 32, 90, 97, 116, 122, 152, 217, 272, 273, 283, 295, 373, 414, 461
KIC1	Protein kinase of the PAK/Ste20 family, required for cell integrity; physically interacts with Cdc31p (centrin), which is a component of the spindle pole body; part of the RAM network that regulates cellular polarity and morphogenesis		S735	CLB2, CDC28		7, 142, 374, 379
CIC1	Essential protein that interacts with proteasome components; has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles	S365; S366	S5	MCK1		32, 100, 370
			S7	MCK1		32, 100, 370
			S10	MCK1		7, 32, 100, 116, 370, 373
			S17	MCK1	PSR1	32, 116, 370, 373, 379
			T11	MCK1	PSR1	7, 32, 100, 116, 370, 373, 379
			T15	MCK1		32, 116, 373, 379
RSC30	Component of the RSC chromatin remodeling complex; non-essential gene required for regulation of ribosomal protein genes and the cell wall/stress response; null mutants are osmosensitive; RSC30 has a paralog, RSC3, that arose from the whole genome duplication	S150; S152	S815	MEC1, TEL1		52

YHR097C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus; YHR097C has a paralog, PAL1, that arose from the whole genome duplication	S221; S222; T223; T224; T225; S233	S222			YVH1	7, 32, 100, 116, 217, 370, 373, 379
			S315	PTK1			7, 32, 56, 116, 142, 152, 373, 379
			T313			PPQ1	7, 32, 116, 142, 152, 373, 379
BZZ1	SH3 domain protein implicated in regulating actin polymerization; able to recruit actin polymerization machinery through its SH3 domains; colocalizes with cortical actin patches and Las17p; interacts with type I myosins	S472	S472	SNF1			7, 32, 142, 374, 379
NVJ1	Nuclear envelope protein; anchored to the nuclear inner membrane, that interacts with the vacuolar membrane protein Vac8p to promote formation of nucleus-vacuole junctions during piecemeal microautophagy of the nucleus (PMN)	S156; S182; T187; S188; S190; S199; T251; S285; S290	S250	SNF1	CKA2		32, 139, 370, 379
			S298	CDC28			7, 116, 142, 217, 373, 379
			T251	SNF1			7, 32, 142, 370, 374, 379
RTS1	B-type regulatory subunit of protein phosphatase 2A (PP2A); Rts1p and Cdc55p are alternative regulatory subunits for PP2A catalytic subunits, Pph21p and Pph22p; PP2A-Rts1p protects cohesin when recruited by Sgo1p to the pericentromere; highly enriched at centromeres in the absence of Cdc55p; required for maintenance of septin ring organization during cytokinesis, for ring disassembly in		S263	YPL150W			32, 152

	G1 and for dephosphorylation of septin, Shs1p; homolog of the mammalian B' subunit of PP2A					
			T242	CDC28		7, 139, 142, 217, 379
FPR3	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; affects expression of multiple genes via its role in nucleosome assembly; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; PPIase domain acts as a transcriptional repressor when tethered to DNA by lexA, and repressor activity is dependent on PPIase activity; FPR3 has a paralog, FPR4, that arose from the whole genome duplication		S80	KSP1	CMP2	7, 32, 37, 116, 142, 152, 217, 373, 433
			S81	KSP1	CMP2	7, 32, 37, 116, 142, 152, 217, 373
			S186	CKA1, CKA2		426
			T89	SSK2		32, 142
			Y184	CKA1, CKA2, CKB1, CKB2	MSG5	243, 425, 426
BFR1	Component of mRNP complexes associated with polyribosomes; involved in localization of mRNAs to P bodies; implicated in secretion and nuclear segregation; multicopy suppressor of BFA (Brefeldin A) sensitivity		T336	CDC28		7, 122, 139, 142, 217, 293, 370, 373, 374
YDR089W; VTC5	Novel subunit of the vacuolar transporter chaperone complex; vacuolar transmembrane protein that regulates biosynthesis of polyphosphate; deletion reduces and overexpression increases polyP accumulation; SPX domain (Syg1, Pho81,	S238; S760	S238	CDC28		142, 370, 374, 379

	Xpr1)-containing protein involved in phosphate homeostasis; relocalizes from vacuole to cytoplasm upon DNA replication stress				
			S324	NNK1	32, 142
			S327	NNK1	7, 32, 116, 142, 217, 373, 374, 379
SEC31	Component of the Sec13p-Sec31p complex of the COPII vesicle coat; COPII coat is required for vesicle formation in ER to Golgi transport; mutant has increased aneuploidy tolerance	T996; S997; S999	S836	CDC28	7, 116, 122, 142, 373, 379
			S974	RAD53	7, 100, 142, 370, 374, 379
			S980	CDC28	7, 32, 100, 142, 374, 379
			S988	KIN82	32, 142, 379
			S992	KIN82	7, 32, 100, 139, 142, 217, 374, 379
HAL5	Putative protein kinase; overexpression increases sodium and lithium tolerance, whereas gene disruption increases cation and low pH sensitivity and impairs potassium uptake, suggesting a role in regulation of Trk1p and/or Trk2p transporters; HAL5 has a paralog, KKQ8, that arose from the whole genome duplication		S64	CDC28	142, 152
			S229	MCK1	32
			S233	MCK1	7, 32, 142, 374, 379
MSS4	Phosphatidylinositol-4-phosphate 5-kinase; involved in actin cytoskeleton organization	T659; S661	S225	PTK1	32, 142, 152, 374, 379

	and cell morphogenesis; multicopy suppressor of stt4 mutation				
			T222	PTK1	32, 37, 142, 152, 217, 374, 379
UME6	Rpd3L histone deacetylase complex subunit; key transcriptional regulator of early meiotic genes; involved in chromatin remodeling and transcriptional repression via DNA looping; binds URS1 upstream regulatory sequence, represses transcription by recruiting conserved histone deacetylase Rpd3p (through co-repressor Sin3p) and chromatin-remodeling factor Isw2p; couples metabolic responses to nutritional cues with initiation and progression of meiosis, forms compl	S316; S318; S321; T403	S107	MCK1, MRK1, RIM11	32, 142, 379, 436
			S316	FRK1	7, 32, 142, 152, 217, 379
			T99	MCK1, MRK1, RIM11	32, 142, 244, 379, 436
			T103	MCK1, MRK1, RIM11	32, 379, 436
AKR1	Palmitoyl transferase involved in protein palmitoylation; acts as a negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; contains ankyrin repeats; AKR1 has a paralog, AKR2, that arose from the whole genome duplication; any of several human homologs encoding DHHC-type zinc fingers (ZDHHC) can complement temperature sensitivity of yeast akr1 null mutant	S51; S57	S57	TPK3	7, 32, 139, 142, 152, 217, 370, 379
YCF1	Vacuolar glutathione S-conjugate transporter; ABC-C transporter of the ATP-binding cassette family; required for	S251; S869; S872; S903	S251	CKA1, CKA2	7, 56, 116, 139, 142, 302, 303,

	vacuole fusion; forms stable complexes with vacuole fusion machinery; regulates Vam7p recruitment to vacuoles; role in detoxifying metals (Cd, Hg, As); transports GSSG that is not immediately reduced in cytosol to vacuole; transports unconjugated bilirubin, selenodigluthatione, oxidized glutathione; similar to human cystic fibrosis protein CFTR					313, 370, 373, 379
			S908	TPK1		7, 88, 139, 142, 152, 217, 302, 370, 374, 379, 382
CAT8	Zinc cluster transcriptional activator; necessary for derepression of a variety of genes under non-fermentative growth conditions, active after diauxic shift, binds carbon source responsive elements; relative distribution to the nucleus increases upon DNA replication stress	S173	S562	SNF1		48
YMR124W; EPO1	Protein involved in septin-ER tethering; interacts with ER membrane protein, Scs2p, and Shs1p, a septin ring component, at bud neck to create ER diffusion barrier; GFP-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; interacts with Crm1p in two-hybrid assay; YMR124W has a paralog, YLR031W, that arose from the whole genome duplication	Y355; S356	S586	CLB2, CDC28		142, 379
TIF4631	Translation initiation factor eIF4G; subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); interacts with Pab1p and with eIF4A (Tif1p); also has a role in biogenesis of the large ribosomal subunit; TIF4631 has a paralog, TIF4632, that arose from the whole genome duplication	S163; S191; S194; S195; S232; T241; T242; T276	S522	KSP1	SIW14	32, 152, 379
TIF4632	Translation initiation factor eIF4G; subunit of the mRNA cap-binding protein complex		T196	CDC28		7, 116, 139, 142, 370,

	(eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); TIF4632 has a paralog, TIF4631, that arose from the whole genome duplication				373, 374, 379
			T301	CDC28	142, 217
RPH1	JmjC domain-containing histone demethylase; targets tri- and dimethylated H3K36; associates with actively transcribed regions and promotes elongation; repressor of autophagy-related genes in nutrient-replete conditions; damage-responsive repressor of PHR1; phosphorylated by the Rad53p-dependent DNA damage checkpoint pathway and by a Rim1p-mediated event during starvation; target of stress-induced hormesis; RPH1 has a paralog, GIS1, that arose from the whole genome duplication	S459; S557; S561; S688; S689	S139	RAD53	52
			S430	CDC28	7, 32, 139, 142, 152, 379
			S561	CDC28	7, 32, 116, 142, 152, 217, 373, 379
			S575	CDC28	7, 142, 379
BEM2	Rho GTPase activating protein (RhoGAP); involved in the control of cytoskeleton organization and cellular morphogenesis; required for bud emergence; potential GAP for Rho4p		T1038	CDC28	142, 379
BOI2	Protein implicated in polar growth, functionally redundant with Boi1p; interacts with bud-emergence protein Bem1p; contains an SH3 (src homology 3) domain and a PH (pleckstrin homology) domain; BOI2 has a paralog, BOI1, that arose from the whole genome duplication	T372; S373; S375; S666; S667	S450	CDC28	32, 142, 217
			S457	CDC28	32, 142, 217

			S519	CDC28	CDC28		7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 374, 379
			S523	CDC28	CDC28		7, 32, 56, 100, 116, 139, 142, 152, 217, 373, 374, 379
			S652	CLB2, CDC28			122, 142, 217, 374, 379
GTT3	Protein of unknown function may be involved in glutathione metabolism; function suggested by computational analysis of large-scale protein-protein interaction data; N- and C-terminal fusion proteins localize to the cell periphery	S116; T120; S121; T123	S116	CTK1			32, 142, 217, 370, 374, 379
ZRG8	Protein of unknown function; authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; GFP-fusion protein is localized to the cytoplasm; transcription induced under conditions of zinc deficiency	S676	S365				32, 56
			S914				142, 379
GIP2	Putative regulatory subunit of protein phosphatase Glc7p; involved in glycogen metabolism; contains a conserved motif (GVNK motif) that is also found in Gac1p, Pig1p, and Pig2p; GIP2 has a paralog, PIG2, that arose from the whole genome duplication		S213	CDC28			142
YER079W	Putative protein of unknown function	T31; S39; S41; Y186; S189; S192; S194; S197; T201	S39		RIM11	SIT4	7, 32, 139, 142, 374

			S41	CDC28	SIT4	7, 32, 142, 374, 379
			S189	TPK3		7, 32, 142, 370, 379
			S192	TPK3		7, 32, 142, 370, 379
			S194	CKA1		7, 32, 142, 379
			T53		SIT4	32
SCS2	Integral ER membrane protein, regulates phospholipid metabolism; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to plasma membrane (PM) and regulate PI4P levels by controlling access of Sac1p phosphatase to substrate PI4P in the PM; interacts with FFAT motifs in Opi1p, Swh1p, Osh2p, and Osh3p; involved in telomeric silencing; VAP homolog; SCS2 has a paralog, SCS22, that arose from the whole genome duplication	T204	T204	CLB2, CDC28		32, 142, 379
SOK1	Protein of unknown function; overexpression suppresses the growth defect of mutants lacking protein kinase A activity; involved in cAMP-mediated signaling; localized to the nucleus; similar to the mouse testis-specific protein PBS13	S193; S197	S191	CDC28		7, 142, 374, 379
			S193	CDC28		7, 116, 142, 373, 374, 379
YTA7	Protein that localizes to chromatin; has a role in regulation of histone gene expression; has a bromodomain-like region that interacts with the N-terminal tail of histone H3, and an ATPase domain; relocalizes to the cytosol in response to hypoxia; potentially phosphorylated by Cdc28p	S11; S1142	S1142	MEC1, TEL1		7, 32, 37, 52, 116, 139, 142, 369, 370, 373, 374, 379

PFK26	6-phosphofructo-2-kinase; inhibited by phosphoenolpyruvate and sn-glycerol 3-phosphate; has negligible fructose-2,6-bisphosphatase activity; transcriptional regulation involves protein kinase A	S42; S43; S667; S671; S673; S674; S675	S652	TPK1			7, 139, 142, 217, 370, 379
			T157	TPK1			7, 56, 82, 142, 217, 370, 379
VHS2	Regulator of septin dynamics; involved in the regulation of septin dynamics at bud neck after mitotic entry, likely by stabilizing septin structure; regulated at post-translational level by cell cycle dependent phosphorylation; likely phosphorylated by Cdc28p and dephosphorylated by Cdc14p before cytokinesis; high-copy suppressor of synthetic lethality of sis2 sit4 double mutant; VHS2 has a paralog, MLF3, that arose from the whole genome duplication		S202			SIT4	32
			S301	CDC28	CDC28		7, 139, 142, 152, 217, 374, 379
			S325			PTP1	32, 142, 152, 217
			S330			PTP1	32, 142, 152
ASG1	Zinc cluster protein proposed to be a transcriptional regulator; regulator involved in the stress response; null mutants have a respiratory deficiency, calcofluor white sensitivity and slightly increased cycloheximide resistance		S166	MEC1, TEL1			7, 52, 370
NUP159	FG-nucleoporin component of central core of the nuclear pore complex; also part of the nuclear pore complex (NPC) cytoplasmic filaments; contributes directly to nucleocytoplasmic transport; regulates ADP release from the ATP-dependent RNA helicase Dbp5p; forms a stable association with Nup82p, Gle2p and two other FG-nucleoporins (Nsp1p and Nup116p)	S402; S404; S940; T948	S182	DUN1			52, 139, 142, 370

			S735	CDC28	7, 116, 122, 142, 217, 370, 373, 379
			S854	CLB2, CDC28	142
MOB1	Component of the mitotic exit network; associates with and is required for the activation and Cdc15p-dependent phosphorylation of the Dbf2p kinase; required for cytokinesis and cell separation; component of the CCR4 transcriptional complex; relocalizes from cytoplasm to the nuclear periphery upon DNA replication stress		S36	CDC28	7, 32, 37, 116, 122, 142, 152, 217, 373, 374, 379
			S80	CLB2, CDC28	7, 32, 37, 100, 139, 142, 217, 370, 374, 379
SLM1	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; TORC2 complex substrate and effector; protein abundance increases in response to DNA replication stress; SLM1 has a paralog, SLM2, that arose from the whole genome duplication	S145; S150	S157	PKH3	32, 370
			S158	PKH3	32, 370
			S659	PKH1, PKH2	67
AIM21	Protein of unknown function; involved in mitochondrial migration along actin filament; may interact with ribosomes; GFP-fusion protein colocalizes with Sac1p to the actin cytoskeleton	S36; T40; T84; S119; T121; T180; S183; S185; S281; T282; S476; S477; T480; T552	S183	PSK2	7, 32, 116, 142, 152, 217, 370, 373, 374, 379

			T180	PSK2	7, 32, 142, 152, 217, 370, 374, 379
BUD6	Actin- and formin-interacting protein; participates in actin cable assembly and organization as a nucleation-promoting factor (NPF) for formins Bni1p and Bnr1p; a triple helical coiled-coil domain in the C-terminal region interacts with Bni1p; involved in polarized cell growth; isolated as bipolar budding mutant; potential Cdc28p substrate	S233	S327	CDC28	7, 12, 32, 116, 142, 217, 370, 373, 374, 379
FKH2	Forkhead family transcription factor; rate-limiting activator of replication origins; evolutionarily conserved regulator of lifespan; binds multiple chromosomal elements with distinct specificities, cell cycle dynamics; positively regulates transcriptional elongation; facilitates clustering, activation of early-firing replication origins; negative role in chromatin silencing at HML and HMR; major role in expression of G2/M phase genes; relocalizes to cytosol under hypoxia		S683	CDC28	225, 312, 379
			S708	CLB2, CDC28	142, 379
			S833	CLB2, CDC28	7, 32, 116, 142, 370, 373, 379
			T697	CDC28	225, 312
GLC8	Regulatory subunit of protein phosphatase 1 (Glc7p); involved in glycogen metabolism and chromosome segregation; proposed to regulate Glc7p activity via conformational alteration; ortholog of the mammalian protein phosphatase inhibitor 2; protein abundance increases in response to DNA replication stress	S184	S158	FRK1	7, 32, 116, 139, 142, 217, 373

MAF1	Highly conserved negative regulator of RNA polymerase III; involved in tRNA processing and stability; inhibits tRNA degradation via rapid tRNA decay (RTD) pathway; binds N-terminal domain of Rpc160p subunit of Pol III to prevent closed-complex formation; regulated by phosphorylation mediated by TORC1, protein kinase A, Sch9p, casein kinase 2; localizes to cytoplasm during vegetative growth and translocates to nucleus and nucleolus under stress conditions	S90	TPK1	7, 32, 142, 203, 267, 374, 379
		S101	TPK1	203, 267, 379
		S159	CKA1, CKA2, CKB1, CKB2	119, 379
		S160	CKA1, CKA2, CKB1, CKB2	119
		S161	CKA1, CKA2, CKB1, CKB2	119
		S162	CKA1, CKA2, CKB1, CKB2	119
		S177	TPK1	32, 56, 142, 152, 203, 267
		S178	TPK1	32, 142, 152, 203, 267, 379
		S179	SCH9	32, 152, 379
		S209	TPK1	142, 203, 217, 267, 374

			S210	TPK1		7, 203, 217, 267
			S388	CKA1, CKA2, CKB1, CKB2		119
VNX1	Calcium/H+ antiporter localized to the endoplasmic reticulum membrane; member of the calcium exchanger (CAX) family; potential Cdc28p substrate	S110; T118; S120; S121	S121	CLB2, CDC28		7, 116, 142, 152, 189, 217, 373, 379
			T118	CLB2, CDC28		142
IES1	Subunit of the INO80 chromatin remodeling complex; relocalizes to the cytosol in response to hypoxia	S504	S36	MEC1, TEL1		7, 52
BLM10	Proteasome activator; binds the core proteasome (CP) and stimulates proteasome-mediated protein degradation by inducing gate opening; required for sequestering CP into proteasome storage granule (PSG) during quiescent phase and for nuclear import of CP in proliferating cells; required for resistance to bleomycin, may be involved in protecting against oxidative damage; similar to mammalian PA200	S11; S29; S34; S35; S36; S62; T64	S11	CDC28		7, 116, 142, 181, 373
			S29	CLB2, CDC28		7, 32, 56, 116, 142, 181, 373, 374, 379
			S56	BUD32		7, 32, 56, 100, 139, 142, 152, 181, 217, 370, 374, 379
YPI1	Regulatory subunit of the type I protein phosphatase (PP1) Glc7p; Glc7p participates in the regulation of a variety of metabolic processes including mitosis and	S133	S131	PSK1	CLA4	7, 32, 37, 56, 116, 139, 142, 217,

	glycogen metabolism; in vitro evidence suggests Ypi1p is an inhibitor of Glc7p while in vivo evidence suggests it is an activator; overproduction causes decreased cellular content of glycogen; partial depletion causes lithium sensitivity, while overproduction confers lithium-tolerance				370, 373, 374
			S133	PSK1	7, 32, 37, 56, 116, 122, 142, 217, 370, 373, 374, 379
IGD1	Cytoplasmic protein that inhibits Gdb1p glycogen debranching activity; required for normal intracellular accumulation of glycogen; phosphorylated in vivo; expression increases during wine fermentation; protein abundance increases in response to DNA replication stress; IGD1 has a paralog, YOL024W, that arose from the whole genome duplication	S14	S95	TPK3	7, 32, 100, 142, 370
LSB3	Protein containing a C-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization; protein abundance increases in response to DNA replication stress; LSB3 has a paralog, YSC84, that arose from the whole genome duplication	T298; S300; S303; S311; S397; S399; T400; S401; S402	S255	CKA1	32
			S256	CKA1	32
CKB1	Beta regulatory subunit of casein kinase 2 (CK2); a Ser/Thr protein kinase with roles in cell growth and proliferation; CK2, comprised of CKA1, CKA2, CKB1 and CKB2, has many substrates including transcription factors and all RNA polymerases	S111	S111	RIO1	7, 32, 152, 370
SUM1	Transcriptional repressor that regulates middle-sporulation genes; required for mitotic repression of middle sporulation-	S378	S379	CDC28	7, 142, 152, 228, 370, 379

	specific genes; also acts as general replication initiation factor; involved in telomere maintenance, chromatin silencing; regulated by pachytene checkpoint						
			S712	MEC1, TEL1			7, 52, 142, 370, 379, 527
			S738	CLB2, CDC28			7, 142, 228, 374, 379
			T306	IME2			3, 271
CTK3	Gamma subunit of C-terminal domain kinase I; CTDK-I phosphorylates RNA polymerase II subunit Rpo21p to affect transcription and pre-mRNA 3' end processing, and also phosphorylates ribosomal protein Rps2p to increase translational fidelity; protein abundance increases in response to DNA replication stress	T34; T35	T34	CTK1			32, 100, 370, 374
MTC1	Protein of unknown function that may interact with ribosomes; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to COPI-coated vesicles (early Golgi); mtc1 is synthetically lethal with cdc13-1	T330; S336; S337; S339; S340; S342	S273		CKA2	YCH1	7, 32, 139, 142, 217, 379
ALY2	Alpha arrestin; controls nutrient-mediated intracellular sorting of permease Gap1p; interacts with AP-1 subunit Apl4p; phosphorylated by Npr1p and also by cyclin-CDK complex Pcl7p-Pho85p; promotes endocytosis of plasma membrane proteins; ALY2 has a paralog, ALY1, that arose from the whole genome duplication	S155; S168; S172; S213; S740; S741	S176	CLB2, CDC28			142
			S213	CDC28			7, 32, 122, 142, 152, 374, 379
NET1	Core subunit of the RENT complex; involved in nucleolar silencing and telophase exit; stimulates transcription by RNA polymerase I and regulates nucleolar	S231	S30	CDC5			363

structure; NET1 has a paralog, TOF2, that arose from the whole genome duplication				
	S31	CDC5		363
	S48	CDC5		236, 363, 379
	S56	CDC5		236
	S60	CDC5		37, 142, 152, 236, 363, 379
	S64	CDC5		152, 236, 363, 379
	S166	CDC28		20, 32, 116, 142, 152, 373, 379
	S169	CDC28		32
	S223	CDC5		363
	S224	CDC5		363
	S228	CDC5	CKA2	7, 37, 139, 142, 152, 236, 363, 374, 379
	S231	CDC5		7, 20, 37, 142, 152, 217, 236, 363, 374, 379
	S242	CDC5		152, 236, 363, 379
	S252	CDC28		7, 20, 32, 37, 122, 142, 152, 236, 379
	S259	CDC5		20, 32, 152, 236, 379
	S269	CDC5		152, 236, 379
	S280	CDC5		236

			S295	CDC5	SNF1	139, 142, 152, 363, 379
			S301	CDC5		363
			S335	CDC5		363
			S447	CLB2, CDC28		32, 37, 142, 379
			S452	CLB2, CDC28		32, 142
			S830	CDC28		7, 32, 37, 142
			S840	RAD53		7, 37, 56, 370, 379
			S1032	CLB2, CDC28	CDC28	7, 20, 32, 116, 139, 142, 217, 373, 374, 379
			S1056	CLB2, CDC28		32, 37, 142, 152, 379
			T16	CDC5		363
			T192	CDC5		236
			T194	CDC5		363
			T195	CDC5		363
			T196	CDC5		363
			T197	CDC5		363
			T288	CDC5		236
			T297	CDC28		142, 152, 363, 379
			T302	CDC5		363
			T676	CLB2, CDC28		20, 32, 56, 142, 152, 217, 374, 379
			T1042	CLB2, CDC28		7, 32, 37, 142, 152, 370, 379
BBC1	Protein possibly involved in assembly of actin patches; interacts with an actin	S77; S78; T81; S83; S103;	S103	CDC28	PHO85	7, 32, 56, 116, 139,

	assembly factor Las17p and with the SH3 domains of Type I myosins Myo3p and Myo5p; localized predominantly to cortical actin patches	S158; S620; S621; T624; T810; S815; T818; T820; S822; T824; T835; T894; T895; S902				142, 217, 370, 373, 374, 379
			S631	MKK1		7, 32, 122, 142, 152, 217, 379
			S634	MKK1		7, 32, 142, 152, 217, 379
			S638	MKK1		32, 116, 122, 142, 152, 217, 373, 379
			T636	MKK1		32, 116, 122, 142, 152, 373, 379
PTK2	Serine/threonine protein kinase; involved in regulation of ion transport across plasma membrane; carboxyl terminus is essential for glucose-dependent Pma1p activation via phosphorylation of Pma1p-Ser899; enhances spermine uptake; PTK2 has a paralog, PTK1, that arose from the whole genome duplication	T56; S57; S59; S61; S63; S65; S69; S73; S585; T586; S587; T588; S592; S595; S711; S726; T727; T729; T730; T732; S773; S775; S776	S69	CLB2, CDC28		37, 142, 152, 379
			S711	PTK2	CKA2	7, 32, 37, 139, 142, 217, 374, 379
			S752	PTK2		7, 32, 116, 142, 217, 373, 374, 379

			S755	PTK2	32, 142, 217, 379
			S784	CLB2, CDC28	7, 32, 37, 142, 379
			T727	CDC28	142, 217
			T730	CDC28	7, 37, 116, 142, 217, 373, 379
			T737	CDC28	116, 142, 217, 373, 379
ENT3	Protein containing an N-terminal epsin-like domain; involved in clathrin recruitment and traffic between the Golgi and endosomes; associates with the clathrin adaptor Gga2p	S148	S203	BUD32	7, 32, 142, 152, 217, 379
ASK10	Regulator of the Fps1p glycerol channel; under nonstress conditions, binds to Fps1p to positively regulate glycerol transport; under osmotic stress, multiple phosphorylation by Hog1p causes Ask10p to dissociate from Fps1p; forms homodimers and heterodimerizes with paralog Rgc1p; phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p; associates with RNA polymerase II holoenzyme	S1070	T808	CDC28	7, 32, 37, 142, 152, 379
GYP7	GTPase-activating protein for yeast Rab family members; members include Ypt7p (most effective), Ypt1p, Ypt31p, and Ypt32p (in vitro); involved in vesicle mediated protein trafficking; contains a PH-like domain		S265	CDC28	142, 379
LYS20	Homocitrate synthase isozyme and functions in DNA repair; catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; LYS20 has a paralog, LYS21, that arose from the whole genome duplication	T396	T396	CDC28	7, 32, 56, 116, 122, 142, 152, 217, 370, 373, 374, 379

YGR237C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	S125; S127	S117			32, 142, 152, 379
TAF4	TFIID subunit (48 kDa); involved in RNA polymerase II transcription initiation; potential Cdc28p substrate	S4; S9; S80	S36	CLB2, CDC28		7, 32, 56, 116, 142, 217, 373
			S49	CDC28		7, 32, 116, 142, 373, 379
PSP2	Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of group II intron-splicing defects of a mutation in MRS2 and of a conditional mutation in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing		S340	CDC28	CDC28	7, 32, 56, 139, 142, 217, 374, 379
SKP1	Evolutionarily conserved kinetochore protein; part of multiple protein complexes, including the SCF ubiquitin ligase complex, the CBF3 complex that binds centromeric DNA, and the RAVE complex that regulates assembly of the V-ATPase; protein abundance increases in response to DNA replication stress	S45; S49	S45	PHO85		32, 142, 152, 379
			S47	PHO85		32, 379
			S49	PTK1		32, 142, 152, 379
			T3	MPS1		37
PYK2	Pyruvate kinase; appears to be modulated by phosphorylation; transcription repressed by glucose, and Pyk2p may be active under low glycolytic flux; PYK2 has a paralog, CDC19, that arose from the whole genome duplication	T374; T378; S379; T380	S24			104
EDC1	RNA-binding protein that activates mRNA decapping directly; binds to mRNA substrate and enhances activity of decapping proteins Dcp1p and Dcp2p; has a role in translation during heat stress; protein becomes more abundant and forms cytoplasmic foci in response to DNA	S82	S82		PTP1	7, 32, 56, 116, 142, 370, 373, 374, 379

	replication stress; EDC1 has a paralog, EDC2, that arose from the whole genome duplication					
			S85		PTP1	32, 116, 142, 373, 374, 379
MDS3	Putative component of the TOR regulatory pathway; negative regulator of early meiotic gene expression; required, with Pmd1p, for growth under alkaline conditions; has an N-terminal kelch-like domain; MDS3 has a paralog, PMD1, that arose from the whole genome duplication	S668; S669; S671; S693; S781; S918; S919; T920; T923; T1156; S1166; T1168	S693	CDC28		7, 32, 37, 116, 142, 217, 370, 373, 374, 379
			S1387	CLB2, CDC28		142, 379
ATG1	Protein serine/threonine kinase; required for vesicle formation in autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; structurally required for phagophore assembly site formation; during autophagy forms a complex with Atg13p and Atg17p; essential for cell cycle progression from G2/M to G1 under nitrogen starvation		S508	TPK1		7, 37, 42, 142, 152, 180, 217, 379, 444, 447
			S515	TPK1		7, 37, 42, 142, 152, 180, 217, 379, 444, 447
INO80	ATPase and nucleosome spacing factor; subunit of complex containing actin and actin-related proteins that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; promotes nucleosome shifts in the 3 prime direction; has a role in modulating stress gene transcription		S102	MEC1, TEL1		52
SDS23	Protein involved in cell separation during budding; one of two S. cerevisiae homologs (Sds23p and Sds24p) of the S. pombe Sds23	S61; T66; S398; S399; S400; S402;	T405	CDC28		142, 217, 379

	protein, which is implicated in APC/cyclosome regulation; SDS23 has a paralog, SDS24, that arose from the whole genome duplication	S404; T405; T409; T410; S430				
YGR054W	Eukaryotic initiation factor eIF2A; associates specifically with both 40S subunits and 80 S ribosomes, and interacts genetically with both eIF5b and eIF4E; homologous to mammalian eIF2A	S473; S560; S561; T563; S564; S567; T568; S572; T581; T586; S587	S560	MCK1	TPK1	7, 32, 139, 142, 370, 374
			S561	MCK1		7, 32, 142, 370, 374
			S564	MCK1		7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			T563	MCK1		7, 32, 116, 142, 152, 217, 370, 373, 374
			T568	MCK1		7, 32, 142, 379
DAM1	Essential subunit of the Dam1 complex (aka DASH complex); cooperates with Duo1p to connect the DASH complex with the microtubules (MT); couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; Ipl1p target for regulating kinetochore-MT attachments		S20	IPL1		49, 139, 142, 177, 254, 374, 379, 392
			S257	IPL1		49, 142, 177, 254, 374, 379
			S265	IPL1		49, 142, 177, 254, 379
			S292	IPL1		49, 142, 177, 374, 379
YGR130C	Component of the eisosome with unknown function; GFP-fusion protein localizes to the	S44; S249; T254; S257;	S343	TPK3		32, 217, 370, 379

	cytoplasm; specifically phosphorylated in vitro by mammalian diphosphoinositol pentakisphosphate (IP7)	T277; T278; S281; S284; S286; T337; S338; T339; T342				
			S347	YPK1		32, 217, 370, 379
DCP2	Catalytic subunit of Dcp1p-Dcp2p decapping enzyme complex; removes 5' cap structure from mRNAs prior to their degradation; also enters nucleus and positively regulates transcription initiation; nudix hydrolase family member; forms cytoplasmic foci upon DNA replication stress; human homolog DCP2 complements yeast dcp2 thermosensitive mutant	S598; S747; S751	S137	STE20		446
HHO1	Histone H1, linker histone with roles in meiosis and sporulation; decreasing levels early in sporulation may promote meiosis, and increasing levels during sporulation facilitate compaction of spore chromatin; binds to promoters and within genes in mature spores; may be recruited by Ume6p to promoter regions, contributing to transcriptional repression outside of meiosis; suppresses DNA repair involving homologous recombination	S130; S173; S174; S176; S177	S130		SIW14	32, 116, 373
FPK1	Ser/Thr protein kinase; phosphorylates several aminophospholipid translocase family members, regulating phospholipid translocation and membrane asymmetry; phosphorylates and inhibits upstream inhibitory kinase, Ypk1p; localizes to the cytoplasm, early endosome/TGN compartments and thplasma membrane; localizes to the shmoo tip where it has a redundant role in the cellular response to mating pheromone; FPK1 has a paralog, KIN82, that arose from the whole genome duplication	S200; S462; T674; S676	S137	CDC28		142, 379

			S140	CDC28		7, 32, 142, 152, 379
			S144	CDC28		32, 142, 152, 379
			S175	CDC28		7, 142
			S198	CDC28		142
			S339	CDC28		7, 142, 152, 370, 379
			T201	CDC28		142
MDG1	Plasma membrane protein; involved in G-protein mediated pheromone signaling pathway; overproduction suppresses bem1 mutations; MDG1 has a paralog, CRP1, that arose from the whole genome duplication	S160; T164; S178; T180; T181; T182; S227; T256; S257; S263; S272	S288	CKA1		7, 32, 116, 122, 142, 152, 373, 374, 379
			S291	PSK2		7, 32, 116, 122, 142, 373, 374, 379
			T290	PSK2		7, 32, 116, 122, 142, 152, 373, 374
BNI5	Linker protein responsible for recruitment of myosin to the bud neck; interacts with the C-terminal extensions of septins Cdc11p and Shs1p and binds Myo1p to promote cytokinesis	S263; S270; S273; T274; T280	S270		SNF1	7, 32, 100, 139, 142, 217, 280, 370, 374, 379
			S273			7, 32, 100, 142, 217, 280, 281, 370, 379
			T274			7, 32, 100, 142, 280, 370, 379
CBK1	Serine/threonine protein kinase of the the RAM signaling network; Ndr/LATS family member; binds regulatory subunit Mob2p; involved in regulation of cellular morphogenesis, polarized growth, and	S63; S66	S570	CBK1		155, 300

	septum destruction; phosphorylation by Cbk1p regulates localization and activity of Ace2p transcription factor and Ssd1p translational repressor; Cbk1p activity is regulated by both phosphorylation and specific localization; relocalizes to cytoplasm upon DNA replication stress				
			T93	CLB2, CDC28	142
			T109	CLB2, CDC28	7, 142, 379
NSG2	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; NSG2 has a paralog, NSG1, that arose from the whole genome duplication	S49; S81; S82	S90	YPK1	7, 32, 100, 142, 152, 217, 370, 374, 379
			S92	YPK1	32, 142, 217, 370, 379
			S93	YPK1	7, 32, 100, 142, 152, 217, 370, 374, 379
CRZ1	Transcription factor, activates transcription of stress response genes; nuclear localization is positively regulated by calcineurin-mediated dephosphorylation; rapidly localizes to the nucleus under blue light stress; can be activated in stochastic pulses of nuclear localization in response to calcium		S409	TPK1	170
			S410	TPK1	142, 170, 370, 379
			S423	TPK1	32, 56, 170
			S427	TPK1	7, 32, 56, 170, 379
			S429	TPK1	7, 32, 170, 379

SUR7	Plasma membrane protein, component of eisosomes; long-lived protein that remains stable in eisosomes of mother cells while other eisosome proteins, Pil1p and Lsp1p, turn over; may function to anchor the eisosome in place; sporulation and plasma membrane sphingolipid content are altered in mutants; localizes to furrow-like invaginations (MCC patches)	T249; T251; S259; S261; S266; S267; T273; S293; S301	S261	TPK3		32, 379
HHT1	Histone H3; core histone protein required for chromatin assembly, part of heterochromatin-mediated telomeric and HM silencing; one of two identical histone H3 proteins (see HHT2); regulated by acetylation, methylation, and phosphorylation; H3K14 acetylation plays an important role in the unfolding of strongly positioned nucleosomes during repair of UV damage		S11	SNF1	GLC7	49, 145, 191, 229, 230, 231
GPD1	NAD-dependent glycerol-3-phosphate dehydrogenase; key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high-osmolarity glycerol response pathway; protein abundance increases in response to DNA replication stress; constitutively inactivated via phosphorylation by the protein kinases Ypk1p and Ypk2p, dephosphorylation increases catalytic activity; forms a heterodimer with Pnc1p to facilitate its peroxisomal import	S23; S24; S25; S27	S24	CTK1		7, 32, 100, 116, 122, 142, 152, 168, 217, 294, 370, 373, 379
			S27	CTK1		7, 32, 100, 116, 122, 142, 152, 168, 217, 294, 370, 373, 374, 379
SLT2	Serine/threonine MAP kinase; coordinates expression of all 19S regulatory particle		S423	RAD53		7, 37, 379, 398

	assembly-chaperones (RACs) to control proteasome abundance; involved in regulating maintenance of cell wall integrity, cell cycle progression, nuclear mRNA retention in heat shock, septum assembly; required for mitophagy, pexophagy; affects recruitment of mitochondria to phagophore assembly site; plays role in adaptive response of cells to cold; regulated by the PKC1-mediated signaling pathway					
			S428	MEC1, TEL1		7, 37, 398
REG1	Regulatory subunit of type 1 protein phosphatase Glc7p; involved in negative regulation of glucose-repressible genes; involved in regulation of the nucleocytoplasmic shuttling of Hxk2p; REG1 has a paralog, REG2, that arose from the whole genome duplication	S254; Y497; S570; S572; S576; T579; S582; S775; T776; S778; Y780; S976; S977; S1013; S1014	S421	CDC28		7, 32, 37, 142, 217, 370, 379
			S898	CDC28		7, 142, 379
			T896	CDC28		142, 379
SED5	cis-Golgi t-SNARE syntaxin; required for vesicular transport between the ER and the Golgi complex; binds at least 9 SNARE proteins		S317	TPK1		171, 422
RSC4	Component of the RSC chromatin remodeling complex; found in close proximity to nucleosomal DNA; displaced from the surface of nucleosomal DNA after chromatin remodeling; acetylated (K25) by Gcn5p, altering replication stress tolerance; contains tandem bromodomains that recognize histone H3 acetylated on K14 (H3K14ac) by Gcn5p		S545	MEC1, TEL1		7, 52, 379
RPL6A	Ribosomal 60S subunit protein L6A; N-terminally acetylated; binds 5.8S rRNA; homologous to mammalian ribosomal protein L6, no bacterial homolog; RPL6A		S12		SIT4	7, 32, 122, 139, 142, 370, 374, 379

	has a paralog, RPL6B, that arose from the whole genome duplication					
MLP1	Myosin-like protein associated with the nuclear envelope; nuclear basket protein that connects the nuclear pore complex with the nuclear interior; involved with Tel1p in telomere length control; involved with Pml1p and Pml39p in nuclear retention of unspliced mRNAs; MLP1 has a paralog, MLP2, that arose from the whole genome duplication	S333; T337	S1670	DUN1		7, 52
			S1675	CDC28		32, 379
			S1710	RAD53		7, 142, 370, 379
			S1723	DUN1		7, 52
VTC3	Regulatory subunit of the vacuolar transporter chaperone (VTC) complex; involved in membrane trafficking, vacuolar polyphosphate accumulation, microautophagy and non-autophagic vacuolar fusion; VTC3 has a paralog, VTC2, that arose from the whole genome duplication	S270; S274; S621; S622	S274		SIT4	7, 32, 116, 142, 152, 373, 379
			S621	CTK1	PPQ1	7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			S622	CTK1	PPQ1	7, 32, 116, 142, 152, 217, 370, 373, 374, 379
			T627	CTK1		7, 32, 116, 142, 373
ROD1	Alpha-arrestin involved in ubiquitin-dependent endocytosis; activating dephosphorylation relays glucose signaling to transporter endocytosis; calcineurin dephosphorylation is required for Rsp5p-	S602; S720	S447	SNF1		11, 361

	dependent internalization of agonist-occupied Ste2p, as part of signal desensitization; recruits Rsp5p to Ste2p via its 2 PPXY motifs; protein abundance increases in response to DNA replication stress; ROD1 has a paralog, ROG3, that arose from the whole genome duplication				
SRP1	Karyopherin alpha homolog; forms a dimer with karyopherin beta Kap95p to mediate import of nuclear proteins, binds the nuclear localization signal of the substrate during import; involved in cotranslational protein degradation; binds ribosome-bound nascent polypeptides; Srp1p and Sts1p couple proteasomes to nascent polypeptides emerging from the ribosome for cotranslational degradation		S67	Kinase CKA1, CKA2	19
SVL3	Protein of unknown function; mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; relocalizes from bud neck to cytoplasm upon DNA replication stress; SVL3 has a paralog, PAM1, that arose from the whole genome duplication	S551	S551	CTK1	7, 32, 122, 142, 152, 217, 370, 374, 379
			T665	PKH3	32
HEH2	Inner nuclear membrane (INM) protein; contains helix-extension-helix (HEH) motif, nuclear localization signal sequence; targeting to the INM requires the Srp1p-Kap95p karyopherins and the Ran cycle; HEH2 has a paralog, SRC1, that arose from the whole genome duplication	S141; S145	S123	CLB2, CDC28	56, 139, 142, 370, 374, 379
PKH3	Protein kinase with similarity to mammalian PDK1 and yeast Pkh1p/Phk2p; yeast Pkh1p and Pkh2p are two redundant upstream activators of Pkc1p; identified as a multicopy suppressor of a pkh1 pkh2 double mutant		S834	PTK2	32, 37, 379

			T832	PTK2		32, 37, 379
STE20	Cdc42p-activated signal transducing kinase; involved in pheromone response, pseudohyphal/invasive growth, vacuole inheritance, down-regulation of sterol uptake; GBB motif binds Ste4p; member of the PAK (p21-activated kinase) family	T203; T207; T216; T408; T411; T413; S418; T546; S547; T552; S924	S206	CDC28		32, 217, 370, 379
			S269		PSR2	32, 116, 373
			S502	CLB2, CDC28		7, 37, 116, 142, 290, 373, 374, 379
			S517	CDC28		32, 37, 56, 142, 370, 379
			S547	CDC28, CLN2		32, 37, 56, 116, 142, 217, 290, 370, 373, 374, 379
			S562	CDC28, CLN2		7, 32, 37, 56, 116, 139, 142, 217, 290, 370, 373, 374, 379
			T203	CLB2, CDC28		7, 32, 142, 217, 370, 379
			T217	CTK1		32, 370, 379
			T218	PKP2		32, 379
			T511	SNF1		32, 37, 142, 370
			T512	CLB2, CDC28		32, 37, 56, 142, 370, 379
			T777	STE20		7, 116, 142, 373, 430
TCB3	Cortical ER protein involved in ER-plasma membrane tethering; one of 6 proteins	S1335; S1340; S1342; S1346;	S1373	CLB2, CDC28		142, 374, 379

	(Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to the plasma membrane (PM) and regulate PM phosphatidylinositol-4-phosphate (PI4P) levels by controlling access of Sac1p phosphatase to its substrate PI4P in the PM; localized to the bud via specific mRNA transport; non-tagged protein detected in a phosphorylated state in mitochondria; C-termini of Tcb1p, Tcb2p and Tcb3p interact	T1347; T1350; S1354; Y1357; S1360; T1364; Y1366; S1371; S1373; T1379; T1382; S1383; S1386				
			T1350	CDC28		7, 32, 100, 122, 142, 152, 217, 331, 370, 374, 379
ESC1	Protein involved in telomeric silencing; required for quiescent cell telomere hypercluster localization at nuclear membrane vicinity; interacts with PAD4-domain of Sir4p	S532	S1145			7, 52, 122, 139, 142, 374, 379
			S1166		PKC1	7, 52, 116, 139, 142, 152, 373
			S1348			32, 370, 379
			S1354			7, 32, 116, 142, 370, 373, 379
			T1353			32, 142, 370, 379
SRC1	Inner nuclear membrane protein; highly enriched at telomeres and subtelomeric regions; functions in regulation of subtelomeric genes and is linked to TREX (transcription export) factors; SRC1 produces 2 splice variant proteins with different functions; alternative splicing of SRC1 pre-mRNA is promoted by Hub1p; mutant has aneuploidy tolerance; SEC1 has a paralog, HEH2, that arose from the whole genome duplication	S181	S80	CLB2, CDC28		7, 142, 217, 370, 374, 379

			S85	CLB2, CDC28	142, 152, 217, 370, 374, 379
			T241	CLB2, CDC28	7, 142, 379
			T291	CLB2, CDC28	116, 139, 142, 370, 373, 379
TAF12	Subunit (61/68 kDa) of TFIID and SAGA complexes; involved in RNA polymerase II transcription initiation and in chromatin modification, similar to histone H2A; overexpression of the human ortholog, TAF12, an oncogene involved in the formation of choroid plexus carcinomas, results in dosage chromosomal instability (dCIN) in a human cell line similar to the dCIN observed in yeast overexpressors		S325	MEC1, TEL1	7, 52, 379
NUP53	FG-nucleoporin component of central core of nuclear pore complex (NPC); also part of the NPC nuclear basket; contributes directly to nucleocytoplasmic transport; involved in regulation of transcription and mitosis; induces membrane tubulation, which may contribute to nuclear pore assembly; NUP53 has a paralog, ASM4, that arose from the whole genome duplication		S101	CDC28	7, 142, 217, 240, 370, 379
			S206	CDC28	240, 379
GIS1	Histone demethylase and transcription factor; regulates genes during nutrient limitation; activity modulated by proteasome-mediated proteolysis; has JmjC and JmjN domain in N-terminus that interact, promoting stability and proper transcriptional activity; contains two transactivating domains downstream of Jmj domains and a C-terminal DNA binding domain; relocalizes to the cytosol in response to hypoxia; GIS1 has a paralog,	S747	S425	CDC28	7, 32, 142, 374

	RPH1, that arose from the whole genome duplication				
			S696	CDC28	7, 142, 217, 370, 374, 379
CUE4	Protein of unknown function; has a CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; CUE4 has a paralog, CUE1, that arose from the whole genome duplication	T32; S41; S48; S54	S48	KNS1	7, 32, 142, 370, 379
SEG1	Component of eisosome required for proper eisosome assembly; precedes Pil1p/Lsp1p during eisosome formation, controls eisosome length and shape; diffusely distributed, forms heterogeneous patches at plasma membrane in small buds, also found in medium and large buds; expression repressed by cAMP; similar to A. gossypii SEG gene and to S. pombe Sle1p, important for generating eisosomes; SEG1 has a paralog, SEG2, that arose from the whole genome duplication	S302; S318; S450; T452	S658	CLB2, CDC28	7, 142, 379
			S870	CDC28	142
			T675	CLB2, CDC28	7, 32, 56, 142, 370, 374, 379
YMR196W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YMR196W is not an essential gene	T1008; S1010; T1013; S1016; S1020	S1081	CDC28	7, 139, 142, 379
BUD22	Protein required for rRNA maturation and ribosomal subunit biogenesis; required for 18S rRNA maturation; also required for small ribosomal subunit biogenesis; cosediments with pre-ribosomal particles; mutation decreases efficiency of +1 Ty1 frameshifting and transposition, and affects budding pattern	T257; T283; T284; S285	T257	SNF1	7, 32, 56, 116, 139, 142, 217, 370, 373, 374, 379

MYO5	One of two type I myosin motors; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; MYO5 has a paralog, MYO3, that arose from the whole genome duplication	S357; Y359; T1034; T1036; S1038; S1040; S1045; T1048; T1051	S357	YPK2		7, 32, 56, 116, 121, 122, 142, 152, 217, 370, 373, 374, 379
UTP14	Subunit of U3-containing Small Subunit (SSU) processome complex; involved in production of 18S rRNA and assembly of small ribosomal subunit	S151	S34		PTC5	7, 32, 142, 152, 217, 370, 379
			S35		PTC5	7, 32, 139, 142, 152, 217, 370, 379
			S488	PTK2		7, 32, 116, 142, 373, 374, 379
			S500	PTK2		7, 32, 116, 142, 370, 373, 379
GAL83	One of three possible beta-subunits of the Snf1 kinase complex; allows nuclear localization of the Snf1 kinase complex in the presence of a nonfermentable carbon source; necessary and sufficient for phosphorylation of the Mig2p transcription factor in response to alkaline stress; functionally redundant with SIP1 and SIP2 for the phosphorylation of Mig1p in response to glucose deprivation; contains a glycogen-binding domain		S64	SNF1		246
			S65	SNF1		246
			S87	CKA1, CKA2, CK1B1, CKB2		246
			S93	CKA1, CKA2,		246

				CK1B1, CKB2			
			T90	CKA1, CKA2, CK1B1, CKB2			246
TRI1	Non-essential sumoylated protein of unknown function; similar to components of human SWI/SNF complex including SMRD3; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, nucleus and nucleolus; TRI1 has a paralog, UAF30, that arose from the whole genome duplication	S113	S113	CDC28	CDC28		7, 139, 142, 379
EIS1	Component of the eisosome required for proper eisosome assembly; similar to Uso1p; authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies; protein increases in abundance and relocalizes from plasma membrane to cytoplasm upon DNA replication stress; EIS1 has a paralog, YKL050C, that arose from the whole genome duplication	T18; S19; S23; S26; S130; S133; S151; S179; S584; S701; Y704; T706; S710; T759; T761; S762; S763; T767; S775; S780; S781; S791; S795; S825; S828; S829; S838	S23			SIW14	32, 56, 116, 142, 370, 373, 379
			S30			SIW14	32
			S130	MCK1	SCH9		7, 32, 56, 116, 139, 142, 152, 331, 373, 374, 379
			S133	MCK1			7, 32, 56, 116, 152, 373, 379
			S136	SNF1			32, 116, 152, 373, 379
			S139	SNF1			32, 379

			S584	YPK1	TPK1		7, 32, 56, 116, 122, 139, 142, 217, 370, 373, 374, 379
			S762	PSK2		YVH1	32, 370, 374
			S763	PKP1		YVH1	7, 32, 116, 142, 152, 370, 373, 374, 379
			S775	CKA1	HRR25		7, 32, 116, 139, 142, 152, 370, 373, 379
			S791	FRK1			32
			T767	PSK2			32, 152, 379
ASM4	FG-nucleoporin component of central core of nuclear pore complex (NPC); contributes directly to nucleocytoplasmic transport; induces membrane tubulation, which may contribute to nuclear pore assembly; ASM4 has a paralog, NUP53, that arose from the whole genome duplication		S464	CDC28			142, 379
MSC3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; msc3 mutants are defective in directing meiotic recombination events to homologous chromatids; potential Cdc28p substrate; protein abundance increases in response to DNA replication stress	S80; S82; S83; T144; S151; S155; Y357; S363; T646; S648; S658; S659; S660	S46	CDC28			142
FPR4	Peptidyl-prolyl cis-trans isomerase (PPIase); nuclear proline isomerase; affects expression of multiple genes via its role in nucleosome assembly; catalyzes isomerization of proline residues in histones H3 and H4, which affects lysine methylation of those histones; PPIase domain acts as a transcriptional repressor	S80; S82	S80	KIN28	CKA2		7, 32, 37, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379

	when tethered to DNA by lexA, and repressor activity is dependent on PPIase activity; contains a nucleoplasmin-like fold and can form pentamers						
			S82	KIN28	CKA2		7, 32, 37, 100, 116, 139, 142, 152, 217, 370, 373, 374, 379
SKG3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate; similar to Skg4p; relocalizes from bud neck to cytoplasm upon DNA replication stress; SKG3 has a paralog, CAF120, that arose from the whole genome duplication	S633	S633	SNF1			32, 56, 116, 217, 373, 379
BCP1	Essential protein involved in nuclear export of Mss4p; Mss4p is a lipid kinase that generates phosphatidylinositol 4,5-biphosphate and plays a role in actin cytoskeleton organization and vesicular transport	T205	T205		CKA2	SIT4	7, 32, 116, 139, 142, 152, 217, 370, 373, 374
ESF1	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels	S86; S372	S86	FUS3			7, 32, 116, 139, 142, 152, 217, 373, 374, 379
			S223			CMP2	7, 32, 116, 139, 142, 217, 373, 374, 379
			T220			CMP2	32, 56, 116, 139, 373, 379
CRN1	Coronin; cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its	S456; S460; S462; S463; S465; S484;	S463			PPH21	7, 32, 56, 116, 142, 217, 370,

	activity; plays a role in regulation of actin patch assembly	S485; T520; T565; S567; S573; T575; S578; S579; T600; S601				373, 374, 379
RSC2	Component of the RSC chromatin remodeling complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; RSC2 has a paralog, RSC1, that arose from the whole genome duplication	S682	S682	CLB2, CDC28	CDC28	7, 32, 116, 122, 139, 142, 152, 217, 373, 374, 379
			T11	MEC1, TEL1		52
			T243	CDC28		7, 32, 142, 374, 379
SPN1	Protein involved in RNA polymerase II transcription; is constitutively recruited to the CYC1 promoter and is required for recruitment of chromatin remodeling factors for the expression of CYC1 gene; interacts genetically or physically with RNAP II, TBP, TFIIS, and chromatin remodelling factors; central domain highly conserved throughout eukaryotes; mutations confer an Spt- phenotype	T15; S85; T86; S89; T120	S23	MEC1, TEL1		7, 32, 52, 116, 142, 152, 217, 370, 373, 374, 379
			S89	SSK2		7, 32, 56, 116, 142, 192, 217, 370, 373, 374, 379
			S118	KNS1		32, 370, 379
YCG1	Subunit of the condensin complex; required for establishment and maintenance of chromosome condensation, chromosome segregation and chromatin binding by the complex; required for tRNA genes clustering at the nucleolus; required for replication slow zone breakage following Mec1p inactivation; transcription is cell cycle regulated, peaking in mitosis and		S16	CDC5		375

	declining in G1; protein is constitutively degraded by the proteasome; rate limiting for condensin recruitment to chromatin				
			S198	CDC5	7, 142, 217, 370, 375, 379
			S902	CDC5	375
			S911	CDC5	375
			S933	CDC5	7, 52, 370, 375, 379
			S964	CDC5	375
			S981	CDC5	7, 56, 374, 375, 379
			S996	CDC5	142, 375, 379
			S1001	CDC5	375, 379
			S1008	CDC5	7, 375
			T941	CDC5	375, 379
			T949	CDC5	375, 379
			T960	CDC5	375
			T979	CDC5	7, 374, 375
NVJ2	Lipid-binding ER protein, enriched at nucleus-vacuolar junctions (NVJ); may be involved in sterol metabolism or signaling at the NVJ; contains a synaptotagmin-like-mitochondrial-lipid binding protein (SMP) domain; binds phosphatidylinositols and other lipids in a large-scale study; may interact with ribosomes, based on co-purification experiments	S591; S621; S622; T624; S640; S646	S676	CDC28	7, 122, 142, 217, 370, 379
SSK1	Cytoplasmic phosphorelay intermediate osmosensor and regulator; part of a two-component signal transducer that mediates osmosensing via a phosphorelay mechanism; required for mitophagy; dephosphorylated form is degraded by the ubiquitin-proteasome system; potential Cdc28p substrate		S195	CDC28	7, 32, 142, 379

			S673	CDC28		32, 56, 116, 142, 217, 373, 379
PEX19	Chaperone and import receptor for newly-synthesized class I PMPs; binds peroxisomal membrane proteins (PMPs) in the cytoplasm and delivers them to the peroxisome for subsequent insertion into the peroxisomal membrane; interacts with Myo2p and contributes to peroxisome partitioning	S301	S62	CKA1		7, 32, 116, 142, 217, 373, 379
HBT1	Shmoo tip protein, substrate of Hub1p ubiquitin-like protein; mutants are defective for mating projection formation, thereby implicating Hbt1p in polarized cell morphogenesis; HBT1 has a paralog, YNL195C, that arose from the whole genome duplication	Y29; S41; S43; T45; S251; T259; S301; S303; Y362; S363; S427; Y428; S431; S795; S843; S850; Y855; S856; S857; S932; T939; T940; S941; Y942; S943; T948; T949; S950; S956; S959; S962; S983; S990; T991; S993; Y1003; S1005; S1036	S41	SAT4		7, 32, 116, 142, 373
			S43	PBS2		32, 116, 142, 373
			S251		SIW14	32
			S257		SIW14	32
			S301	PSK2		32, 142
			S303	MCK1		32, 142, 370, 374
			S363	PKP1	PPH22	7, 32, 56, 116, 142, 370, 373

			S561		PPH22	32, 142
			S671	CDC28	PPS1	32, 142
			S856	PKP1		32, 142
			S857	MCK1	PPH22	32, 142, 374
			S956	MCK1		7, 32, 100, 116, 142, 370, 373, 374
			S959	MCK1	PPH22	32, 100, 116, 142, 373, 374
			S962	PKP1	PPH22	32, 100, 116, 142, 373, 374
			S990	CMK1		32
			S1034	PKP1	CLA4	7, 32, 116, 122, 139, 142, 217, 373
			S1036	CLA4	PPH22	7, 32, 116, 122, 142, 373
			T366	PSK2		7, 32, 370
			T368	PKP1		32
			T949	PBS2		32
			T991	PKP1		32
			T997	MCK1		32, 56, 100, 142
			Y362	PBS2		32
			Y987	MCK1		32
VPS13	Protein involved in prospore membrane morphogenesis; peripheral membrane protein that localizes to the prospore membrane and at numerous membrane contact sites; involved in sporulation, vacuolar protein sorting, prospore membrane formation during sporulation, and protein-Golgi retention; required for mitochondrial integrity; contains a PH-like	T433; S436; T438; T440	S1715	RCK2	PKC1	7, 32, 122, 139, 142, 217, 370, 379

	domain; homologous to human CHAC and COH1 which are involved in Chorea-acanthocytosis and Cohen syndrome, respectively					
			T1379	CDC28	CDC28	7, 32, 100, 139, 142, 379
ZEO1	Peripheral membrane protein of the plasma membrane; interacts with Mid2p; regulates the cell integrity pathway mediated by Pkc1p and Slt2p; the authentic protein is detected in a phosphorylated state in highly purified mitochondria	S40; T49	S85	BUD32		32, 116, 152, 373
			S89	PTK1		32, 116, 152, 373, 379
			T49	VPS34		7, 32, 56, 116, 122, 139, 142, 217, 331, 370, 373, 379
RTC1	Subunit of SEACAT, a subcomplex of the SEA complex; Rtc1p, along with Mtc5p and Sea4p, redundantly inhibit the TORC1 inhibitory role of the Iml1p/SEACIT (Iml1p-Npr2p-Npr3p) subcomplex, a GAP for GTPase Gtr1p (EGOC subunit) in response to amino acid limitation, thereby resulting in activation of TORC1 signaling; SEA is a coatomer-related complex that associates dynamically with the vacuole; has N-terminal WD-40 repeats and a C-terminal RING motif; null suppresses cdc13-1		S946	SNF1		7, 32, 142, 370, 379
			S950	SNF1		7, 32, 116, 142, 217, 370, 373, 379
CUE5	Ubiquitin-binding protein; functions as ubiquitin-Atg8p adaptor in ubiquitin-	S21; S36; S45; T50; T70;	S21	MKK1		7, 32, 116, 142, 217,

	dependent autophagy; serves as proteaphagy receptor for inactivated 26S proteasomes; contains CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; CUE5 has a paralog, DON1, that arose from the whole genome duplication; human TOLLIP is a functional CUE-domain homolog, can complement yeast null mutant, rescuing hypersensitivity of cue5 null mutant cells to Htt-96Q	S220; T346; S348; S351; T352			370, 373, 379
			S220	KSP1	7, 32, 142, 217, 374, 379
			T364	CLB2, CDC28	7, 32, 100, 116, 142, 152, 217, 370, 373, 379
			T367	CDC28	32, 100, 142, 152, 370, 379
			T369	CDC28	7, 32, 152
VHS3	Negative regulatory subunit of protein phosphatase 1 Ppz1p; involved in coenzyme A biosynthesis; subunit of the phosphopantothenoylcysteine decarboxylase (PPCDC; Cab3p, Sis2p, Vhs3p) complex and the CoA-Synthesizing Protein Complex (CoA-SPC: Cab2p, Cab3p, Cab4p, Cab5p, Sis2p and Vhs3p)	T108; T183; S221; S223; T224; S225	S223	RTK1	7, 32, 142, 217
			S225	CDC28	7, 32, 142, 374
ALE1	Broad-specificity lysophospholipid acyltransferase; part of MBOAT family of membrane-bound O-acyltransferases; key component of Lands cycle; may have role in fatty acid exchange at sn-2 position of mature glycerophospholipids	S513	S513	PHO85	7, 32, 56, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
HRK1	Protein kinase; implicated in activation of the plasma membrane H(+)-ATPase Pma1p		S47	HRK1	7, 32, 152, 370

	in response to glucose metabolism; plays a role in ion homeostasis; protein abundance increases in response to DNA replication stress					
TCO89	Subunit of TORC1 (Tor1p or Tor2p-Kog1p-Lst8p-Tco89p); regulates global H3K56ac; TORC1 complex regulates growth in response to nutrient availability; cooperates with Ssd1p in the maintenance of cellular integrity; deletion strains are hypersensitive to rapamycin	S119; S546	S497	PTK2		32, 142, 379
			S500	PTK2		32, 142, 379
			S546	CLB2, CDC28		116, 142, 217, 373, 379
SLF1	RNA binding protein that associates with polysomes; may be involved in regulating mRNA translation; involved in the copper-dependent mineralization of copper sulfide complexes on cell surface in cells cultured in copper salts; SLF1 has a paralog, SRO9, that arose from the whole genome duplication; protein abundance increases in response to DNA replication stress	S40; S41; S42	S42	CDC28		7, 32, 122, 142, 374, 379
RCN2	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; phosphorylated in response to alpha factor; protein abundance increases in response to DNA replication stress	S102; S104; T105; S110; S129; T132; S149; S150; S152; S156; S157; S160; S183; S185; S186; S187; S188; T189; T200; S201; S204; T248; S250; S255; S257; T259	S143	SLT2		32
			S150	SLT2	RIM11	7, 32, 100, 116, 122, 139, 142,

						152, 217, 370, 373, 374, 379
			S152	TPK2		7, 32, 100, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S157	TPK2		7, 32, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S160	SLT2		7, 32, 100, 116, 122, 142, 152, 217, 370, 373, 374, 379
			T132	TPK2		7, 32, 142, 217, 370
IOC2	Subunit of the Isw1b complex; exhibits nucleosome-stimulated ATPase activity and acts within coding regions to coordinate transcription elongation with termination and processing; contains a PHD finger motif; other complex members are Isw1p and Ioc4p		S262	MEC1, TEL1		7, 52, 142, 379
			S605	MEC1, TEL1		52
			S760	MEC1, TEL1		52
CHS5	Component of the exomer complex; the exomer which also contains Csh6p, Bch1p, Bch2p, and Bud7, is involved in the export of select proteins, such as chitin synthase Chs3p, from the Golgi to the plasma membrane; interacts selectively with the	S312; S318; S321; S338; S347; T348; S365; T373; S384; S399;	S347		SIT4	32, 370

	activated, GTP-bound form of Arf1p; Chs5p is the only protein with a BRCT domain that is not localized to the nucleus	S400; S579; S590; S600					
			T334			SIT4	32, 142, 370, 379
MRH1	Protein that localizes primarily to the plasma membrane; also found at the nuclear envelope; long-lived protein that is asymmetrically retained in the plasma membrane of mother cells; the authentic, non-tagged protein is detected in mitochondria in a phosphorylated state; null mutation confers sensitivity to acetic acid	S289; T295; S299	S289	YPK1	CDC28	SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
			T295	PSK2	CDC28	SIT4	7, 32, 56, 100, 116, 122, 139, 142, 152, 217, 331, 370, 373, 374, 379
LYS21	Homocitrate synthase isozyme; catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; LYS21 has a paralog, LYS20, that arose from the whole genome duplication	S409; T410	T410	CDC28			7, 32, 56, 116, 142, 217, 370, 373, 374
DCS2	m(7)GpppX pyrophosphatase regulator; non-essential, stress induced regulatory protein; modulates m7G-oligoribonucleotide metabolism; inhibits Dcs1p; regulated by Msn2p, Msn4p, and the Ras-cAMP-cAPK signaling pathway; mutant has increased aneuploidy tolerance; DCS2 has a paralog, DCS1, that arose from the whole genome duplication	S58; S60; S63; T64; T340; S341	S63	PKH2			7, 32, 142, 370, 374
			T64	MCK1			7, 32, 116, 142, 370, 373, 374

MSL5	Component of commitment complex; which defines first step in splicing pathway; essential protein that interacts with Mud2p and Prp40p, forming a bridge between the intron ends; also involved in nuclear retention of pre-mRNA; relocalizes to the cytosol in response to hypoxia	S93; S95; S376; S378	S376	CDC28		7, 32, 142, 152, 370, 379
			S378	CDC28		7, 32, 142, 152, 370, 379
BUG1	Cis-golgi localized protein involved in ER to Golgi transport; forms a complex with the mammalian GRASP65 homolog, Grh1p; mutants are compromised for the fusion of ER-derived vesicles with Golgi membranes	S2; S87; T275; T277	S87	CKA2		7, 32, 116, 139, 142, 217, 370, 373, 374, 379
			T277	CDC28		142, 379
RLM1	MADS-box transcription factor; component of the protein kinase C-mediated MAP kinase pathway involved in the maintenance of cell integrity; phosphorylated and activated by the MAP-kinase Slt2p; RLM1 has a paralog, SMP1, that arose from the whole genome duplication		S427	SLT2		169
			T439	SLT2		169
INP53	Polyphosphatidylinositol phosphatase; dephosphorylates multiple phosphatidylinositol phosphates; involved in trans Golgi network-to-early endosome pathway; hyperosmotic stress causes translocation to actin patches; contains Sac1 and 5-ptase domains; INP53 has a paralog, INP52, that arose from the whole genome duplication	S986; T988	S986	CDC28	PHO85	7, 32, 37, 116, 139, 142, 370, 373, 374, 379
			T988	CLB2, CDC28		7, 32, 142, 374
HER1	Protein of unknown function; required for proliferation or remodeling of the ER that is caused by overexpression of Hmg2p; may interact with ribosomes, based on co-purification experiments; HER1 has a	S277; S280; S1013; S1204	S61	CDC28		142, 379

	paralog, GIP3, that arose from the whole genome duplication						
			T128	SNF1			32, 56, 142, 379
MAM3	Protein required for normal mitochondrial morphology; has similarity to hemolysins	S434; S435; S439; S475; T477; T485; T575; T599	S522	MCK1			32, 142
			S523	MCK1			32, 56, 142
			S527	MCK1			32, 56, 116, 142, 373, 379
			T519	MCK1			32, 56, 142, 379
HSP42	Small heat shock protein (sHSP) with chaperone activity; forms barrel-shaped oligomers that suppress unfolded protein aggregation; involved in cytoskeleton reorganization after heat shock; protein abundance increases and forms cytoplasmic foci in response to DNA replication stress	S182; S213; S214; S215; S223; S232; T236	S213	PBS2	TPK1		7, 32, 139, 142, 152, 217, 370, 379
			S214	PBS2	SNF1	PPH21	7, 32, 116, 122, 139, 142, 152, 217, 370, 373, 379
			S215			PPH21	7, 32, 116, 122, 142, 152, 217, 370, 373, 379
			S223			PPH21	7, 32, 142, 379
WHI5	Repressor of G1 transcription; binds to SCB binding factor (SBF) at SCB target promoters in early G1; dilution of Whi5p concentration during cell growth determines cell size; phosphorylation of Whi5p by the CDK, Cln3p/Cdc28p relieves repression and promoter binding by Whi5, and contributes	T284; S288	S59				7, 32, 68, 116, 122, 142, 152, 370, 373, 379, 416

	to both the determination of critical cell size at START and cell fate; periodically expressed in G1					
			S62			7, 32, 68, 116, 122, 142, 152, 370, 373, 379, 416
			S88			142, 152, 416
			S154			7, 32, 68, 142, 152, 379, 384, 416
			S156			7, 32, 68, 142, 152, 370, 379, 384, 416
			S161			7, 32, 68, 142, 152, 370, 379, 384, 416
			T5			68, 189, 416
			T57	CDC28		32, 68, 139, 142, 152, 370, 379, 416
STB3	Ribosomal RNA processing element (RRPE)-binding protein; involved in the glucose-induced transition from quiescence to growth; restricted to nucleus in quiescent cells, released into cytoplasm after glucose repletion; binds Sin3p; relative distribution to the nucleus increases upon DNA replication stress	S9; S307	S337		PTC7	32, 142, 152, 374, 379
			S341		PTC7	32, 56, 152, 379
POM34	Subunit of the transmembrane ring of the nuclear pore complex (NPC); contributes to nucleocytoplasmic transport, NPC		T221	CLB2, CDC28		142, 379

	biogenesis and spindle pole body duplication						
			T273	CDC28			142, 217, 379
PAR32	Protein of unknown function; hyperphosphorylated upon rapamycin treatment in a Tap42p-dependent manner; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; PAR32 is not an essential gene		S36	PHO85	SNF1		7, 32, 37, 116, 122, 139, 142, 152, 217, 370, 373, 374, 379
			S39	PHO85			7, 32, 37, 116, 122, 142, 152, 217, 370, 373, 374, 379
			S49	PHO85			32, 152
			S131	VPS15			32
			S138			YCH1	32, 142, 152, 217, 374, 379
			S141			YCH1	32, 37, 142, 152, 217, 370, 379
			S148	CLB2, CDC28			7, 32, 142, 152
			S246	CLB2, CDC28	CDC28		7, 32, 116, 122, 139, 142, 152, 217, 373, 374, 379
ENT1	Epsin-like protein involved in endocytosis and actin patch assembly; functionally redundant with Ent2p; binds clathrin via a clathrin-binding domain motif at C-terminus; relocalizes from bud neck to cytoplasm upon DNA replication stress; ENT1 has a paralog, ENT2, that arose from the whole genome duplication	T160; S163	T346	PRK1			7, 56, 116, 146, 370, 373, 374, 379

			T366	PRK1			7, 142, 146, 217, 379
			T395	PRK1			7, 122, 142, 146, 152, 217, 370, 379, 421
			T415	PRK1			421
			T427	PRK1			146
CSR2	Nuclear ubiquitin protein ligase binding protein; may regulate utilization of nonfermentable carbon sources and endocytosis of plasma membrane proteins; overproduction suppresses chs5 spa2 lethality at high temp; ubiquitinated by Rsp5p, deubiquitinated by Ubp2p; CSR2 has a paralog, ECM21, that arose from the whole genome duplication	S1007	S963	CDC28			142
HRP1	Subunit of cleavage factor I; cleavage factor I is a five-subunit complex required for the cleavage and polyadenylation of pre-mRNA 3' ends; RRM-containing heteronuclear RNA binding protein and hnRNPA/B family member that binds to poly (A) signal sequences; required for genome stability	S2; S87	S462	CDC28			7, 32, 116, 122, 142, 373, 379
IGO2	Protein required for initiation of G0 program; prevents degradation of nutrient-regulated mRNAs via the 5'-3' mRNA decay pathway; phosphorylated by Rim15p; GFP protein localizes to the cytoplasm and nucleus; IGO2 has a paralog, IGO1, that arose from the whole genome duplication		S119		CLA4	PPH22	32, 139, 142, 379
			S122			PPH22	32, 142, 152, 370, 379
			S128	CLB2, CDC28			32, 142, 152, 370, 379

Table 3.7 Phosphorylated proteins and their kinases and phosphatases in high and low density cells treated with LCA at day 7.

Reference Number	iPTM Format	Reference Number	iPTM Format	Reference Number	iPTM Format	Reference Number	iPTM Format
1	1170432	**116**	19795423	**232**	30578283	**347**	16684773
2	25569479	**117**	11170432	**233**	11720288	**348**	20046099
3	19528232	**118**	29905868	**234**	14519092	**349**	31368600
4	15652479	**119**	21383183	**235**	21532587	**350**	27821475
5	15970663	**120**	31209110	**236**	12096118	**351**	8325852
6	17178716	**121**	16478726	**237**	9600950	**352**	7523111
7	18407956	**122**	15665377	**238**	17239901	**353**	23754852
8	18407950	**123**	16990850	**239**	18391019	**354**	16776651
9	21317875	**124**	19564916	**240**	17461799	**355**	30546002
10	10428955	**125**	28076776	**241**	22984552	**356**	8670804
11	26920760	**126**	9737955	**242**	7624781	**357**	31399582
12	20020052	**127**	18287090	**243**	15358193	**358**	24803522
13	12141686	**128**	14988503	**244**	9372955	**359**	23363605
14	31331965	**129**	26439012	**245**	15240832	**360**	16890524
15	20368617	**130**	1187543	**246**	19897735	**361**	17949685
16	20520775	**131**	16230527	**247**	2834362	**362**	26447709
17	15145958	**132**	18854322	**248**	12823808	**363**	11960554
18	25523922	**133**	8226915	**249**	22290438	**364**	19578373
19	9258433	**134**	15781691	**250**	22019086	**365**	26711254
20	15273393	**135**	22213798	**251**	11486005	**366**	31009484
21	15548536	**136**	23707760	**252**	21996927	**367**	10403407
22	19398558	**137**	21931684	**253**	17106258	**368**	17531808
23	16168390	**138**	9047292	**254**	15108802	**369**	15972895
24	17892487	**139**	21126336	**255**	26179915	**370**	17563356
25	16118184	**140**	25183013	**256**	29237818	**371**	24947305
26	20876143	**141**	19269975	**257**	27068241	**372**	17853895
27	16362369	**142**	19779198	**258**	2722821	**373**	19823750
28	12917340	**143**	12847291	**259**	19731963	**374**	20702584
29	9718324	**144**	24019977	**260**	7905477	**375**	19481522
30	12637550	**145**	10975519	**261**	19008353	**376**	22564307
31	10805732	**146**	13679512	**262**	20399186	**377**	19805182
32	21177495	**147**	17303466	**263**	23471970	**378**	24876385
33	17522259	**148**	8754836	**264**	26394309	**379**	23749301
34	29895620	**149**	9584169	**265**	24096659	**380**	16085488
35	21135117	**150**	22319457	**266**	19221193	**381**	16829593
36	9414109	**151**	16844690	**267**	17005718	**382**	7521334
37	20489023	**152**	19684113	**268**	20159553	**383**	20170726
38	20702586	**153**	17213332	**269**	21419342	**384**	19713766

39	19692334	**154**	3537803	**270**	21576760	**385**	20471941
40	20826609	**155**	17145962	**271**	17198398	**386**	28600888
41	21311222	**156**	19962308	**272**	26356805	**387**	11756670
42	16172400	**157**	15296722	**273**	28496991	**388**	12407105
43	18086883	**158**	16940359	**274**	22918958	**389**	12429908
44	1316274	**159**	14735355	**275**	29038496	**390**	19901073
45	20823268	**160**	22323608	**276**	9308187	**391**	11344302
46	10074427	**161**	27261458	**277**	26274562	**392**	20479468
47	29438499	**162**	3299046	**278**	31455721	**393**	3037314
48	15121831	**163**	26728856	**279**	30856163	**394**	29352143
49	12408861	**164**	30044722	**280**	17342053	**395**	15711538
50	24302356	**165**	22031224	**281**	17618228	**396**	9774644
51	17114794	**166**	23861665	**282**	1961721	**397**	16428446
52	20190278	**167**	31323064	**283**	11734846	**398**	19805511
53	26682552	**168**	20026609	**284**	12748292	**399**	23217712
54	30516470	**169**	12410835	**285**	28166236	**400**	29727620
55	15823538	**170**	15470242	**286**	22307609	**401**	16292314
56	17287358	**171**	21987636	**287**	9725902	**402**	22889169
57	11751637	**172**	16055732	**288**	11080154	**403**	22447937
58	21081492	**173**	19995911	**289**	16968695	**404**	15610741
59	20145252	**174**	20383061	**290**	10359756	**405**	7608180
60	22334681	**175**	10816418	**291**	22573892	**406**	17560372
61	22638969	**176**	21841122	**292**	23468521	**407**	16135807
62	16294044	**177**	19923271	**293**	795423	**408**	25492886
63	19860830	**178**	16299494	**294**	23149688	**409**	15607975
64	14756785	**179**	22289182	**295**	12553912	**410**	16109375
65	16777072	**180**	20953146	**296**	19779190	**411**	7742363
66	12502746	**181**	20486117	**297**	25073408	**412**	8102207
67	17101780	**182**	16844691	**298**	15870265	**413**	23230424
68	15210110	**183**	21212735	**299**	9523726	**414**	9334303
69	11807089	**184**	8243648	**300**	19967545	**415**	21531713
70	16751660	**185**	17914457	**301**	17588515	**416**	19172996
71	19269952	**186**	15127225	**302**	18667437	**417**	19805817
72	18413716	**187**	19684110	**303**	22449970	**418**	19220811
73	1977585	**188**	21993622	**304**	1956339	**419**	16308562
74	23184661	**189**	19520826	**305**	7489717	**420**	11113180
75	18818768	**190**	8286332	**306**	19021767	**421**	11694597
76	1739968	**191**	16980586	**307**	20815814	**422**	16093353
77	10556086	**192**	12242279	**308**	12872131	**423**	10527941

78	14607111	**193**	16756761	**309**	29719209	**424**	9228053
79	8200534	**194**	9001236	**310**	26582917	**425**	7559654
80	19801655	**195**	19150427	**311**	28510759	**426**	9148902
81	11724581	**196**	22031291	**312**	15509804	**427**	10490639
82	12755632	**197**	19429778	**313**	20812950	**428**	28841133
83	15037628	**198**	30377154	**314**	15024067	**429**	9753544
84	9032272	**199**	24198248	**315**	28143980	**430**	7608157
85	11140636	**200**	20386698	**316**	6324168	**431**	9388196
86	10837245	**201**	16342953	**317**	16426231	**432**	14555477
87	16977319	**202**	17932035	**318**	1831768	**433**	21725298
88	15556603	**203**	19299514	**319**	16612003	**434**	9032256
89	16510118	**204**	22364741	**320**	22124158	**435**	16166626
90	15448699	**205**	25970584	**321**	21078689	**436**	10891485
91	8943257	**206**	8386319	**322**	1448107	**437**	20388513
92	1468623	**207**	21255108	**323**	21070963	**438**	16854988
93	18267004	**208**	30610170	**324**	9566913	**439**	20932477
94	20951350	**209**	18851834	**325**	1613787	**440**	28575419
95	25344756	**210**	16467380	**326**	7634071	**441**	24130459
96	21280672	**211**	19411703	**327**	18256024	**442**	12215532
97	9346239	**212**	27621363	**328**	11877433	**443**	20439775
98	8035796	**213**	1092346	**329**	23645671	**444**	21460632
99	27050455	**214**	10094396	**330**	9744870	**445**	21712380
100	11875433	**215**	28739659	**331**	17761666	**446**	20513766
101	2034654	**216**	9671029	**332**	3005313	**447**	17699586
102	19795420	**217**	17330950	**333**	3038868	**448**	12477803
103	11278681	**218**	12695666	**334**	9843429	**449**	20948969
104	20639203	**219**	25049391	**335**	15470109	**450**	10952997
105	18980262	**220**	21296759	**336**	19966303	**451**	9398162
106	19780626	**221**	23468650	**337**	22080611	**452**	7592868
107	21954159	**222**	7592925	**338**	28069741	**453**	9885245
108	1332607	**223**	8703213	**339**	17545469	**454**	17898076
109	18084032	**224**	24842996	**340**	17991748	**455**	10679022
110	18180296	**225**	28649434	**341**	21464305	**456**	26899143
111	25778921	**226**	15840588	**342**	12372297	**457**	18791219
112	23894419	**227**	19581288	**343**	17563350	**458**	11283598
113	25595672	**228**	22106412	**344**	24968058	**459**	8798780
114	11233987	**229**	10911986	**345**	17137646	**460**	20825495
115	14759366	**230**	11498592	**346**	14612412	**461**	17302822

Table 3.8 List of references displayed in Tables 3.3-3.7 and their associated PMIDs.